

78206

3-612

217967

STIC-Biotech/ChemLib CRFD

From: Chan, Christina  
Sent: Monday, March 12, 2007 11:41 AM  
To: Li, Bao-Qun; STIC-Biotech/ChemLib  
Subject: RE: 10789355

Please rush. Thanks Chris

Chris Chan  
TC 1600 New Hire Training Coordinator and SPE 1644  
(571)-272-0841  
Remsen, 3E89

3C18

-----Original Message-----

From: Li, Bao-Qun  
Sent: Monday, March 12, 2007 9:13 AM  
To: Chan, Christina; STIC-Biotech/ChemLib  
Subject: 10789355

Please prove the rush order of alignment analysis of SEQ ID NO: 5 with SEQ ID NO: 2, 4, 6, 7, and 25.  
Thank you.

Bao Qun Li M.D  
TC 1600  
Art Unit 1648  
Tel. 517-272-0904  
REM. 3C18  
Rm. 3D24

2 Na 8642  
4 Na 8643  
6 Na 8638  
7 Na 8638  
25 Na 8638

119

my

3/12/2007

Qy	5822	GGGCTCAATCAATACATGGTTGGGTACAGCTCCCTCGAGAGCCGAAACGGACGTAGCA	5881
Db	5822		
Qy	5882	GGGCTCAATCAATACCGGTTGGGTACAGCTCCCTCGAGAGCCGAACTGGAGCTAGCA	5881
Db	5882		
Qy	5882	GTGCTCATCTTCATGTCTACCGACCCCTCCACATTACGGCGGAGACGGCTAAGCGTAGG	5941
Db	5882	GTGCTCATCTTCATGTCTACCGACCCCTCCACATTACGGCGGAGACGGCTAAGCGTAGG	5941
Qy	5942	CTGGCAGGGGATCTCCCTCTCTGGCCAGCTCATCAGTACGAGCTGTCTGGCCC	6001
Db	5942	CTGGCAGGGGATCTCCCTCTCTGGCCAGCTCATCAGTACGAGCTGTCTGGCCCT	6001
Qy	6002	TCCTTGAAGCAACATGCACTACCCGTCATGACTCCCGGACGCTGACCTCATCGAGGCC	6061
Db	6002	TCCTTGAAGCAACATGCACTACCCGTCATGACTCCCGGACGCTGACCTCATCGAGGCC	6061
Qy	6062	AACCTCTCTGTGGGCGCAGGAGATGGGCGGGAACATCACCCGCTGGAGTCAGAGAAATAAG	6121
Db	6062	AACCTCTCTGTGGGCGCAGGAGATGGGCGGGAACATCACCCGCTGGAGTCAGAGAAATAAG	6121
Qy	6122	GTAGTAATTTTGGACTCTTTCGAGCCGCTCAAGCGGAGGAGATGAGAGGGAAGTATCC	6181
Db	6122	GTAGTAATTTTGGACTCTTTCGAGCCGCTCAAGCGGAGGAGATGAGAGGGAAGTATCC	6181
Qy	6182	GTTCGGCGGAGATCTCGCGGAGTCCAGGAAATTCCTCGAGCATGCCCATATGGGCA	6241
Db	6182	GTTCGGCGGAGATCTCGCGGAGTCCAGGAAATTCCTCGAGCATGCCCATATGGGCA	6241
Qy	6242	CGCCCGGATTTACAACTCTTACCTGTTAGAGTCTCTGGAAGACCCGGACTACGTCCTTCCA	6301
Db	6242	CGCCCGGATTTACAACTCTTACCTGTTAGAGTCTCTGGAAGACCCGGACTACGTCCTTCCA	6301
Qy	6302	GTGGTACACGGGTGTCTCAATTCGCGCTCCCAAGCCCTCCGATACCACTCCACGGAGG	6361
Db	6302	GTGGTACACGGGTGTCTCAATTCGCGCTCCCAAGCCCTCCGATACCACTCCACGGAGG	6361
Qy	6362	AAGAGGACGTGTCTGTCAGAACTACCGTGTCTTCTGCTTGGCGGAGCTCGCCACA	6421
Db	6362	AAGAGGACGTGTCTGTCAGAACTACCGTGTCTTCTGCTTGGCGGAGCTCGCCACA	6421
Qy	6422	AAGACCTTCGGCAGCTCCGAATCGTCGCGCTCGACAGCGGCACGCAACGGCTCTCTCT	6481
Db	6422	AAGACCTTCGGCAGCTCCGAATCGTCGCGCTCGACAGCGGCACGCAACGGCTCTCTCT	6481
Qy	6482	GACAGCCCTCCGACAGCGGAGCGGGATCGAAGTTCGATGCTGCTCATGCCC	6541
Db	6482	GACAGCCCTCCGACAGCGGAGCGGGATCGAAGTTCGATGCTGCTCATGCCC	6541
Qy	6542	CCCTTGAAGGGGAGCGGGGATCCCGATCTCAGCGAGCGGTCTTGGTCTACCGTAAGC	6601
Db	6542	CCCTTGAAGGGGAGCGGGGATCCCGATCTCAGCGAGCGGTCTTGGTCTACCGTAAGC	6601
Qy	6602	GAGGAGCTAGTGAGGACGTCTGCTGCTGCTCGATGCTTACACATGACAGCGGCCCTG	6661
Db	6602	GAGGAGCTAGTGAGGACGTCTGCTGCTGCTCGATGCTTACACATGACAGCGGCCCTG	6661
Qy	6662	ATCAGCCCATCTCGCTCGGAGGAAACCAAGTGGCCATCAATGCACTGAGCAACTCTTTG	6721
Db	6662	ATCAGCCCATCTCGCTCGGAGGAAACCAAGTGGCCATCAATGCACTGAGCAACTCTTTG	6721
Qy	6722	CTCGTCAACCAACTTGTGTATGTACACATCTCGACGCCCAAGCCTGCGGCAAG	6781
Db	6722	CTCGTCAACCAACTTGTGTATGTACACATCTCGACGCCCAAGCCTGCGGCAAG	6781
Qy	6782	AAGGTCACTTTGACAGCTGACGCTCTGGAACCACTACCGGACGCTGCTCAAGGAG	6841
Db	6782	AAGGTCACTTTGACAGCTGACGCTCTGGAACCACTACCGGACGCTGCTCAAGGAG	6841
Qy	6842	ATGAAGCGAAGCGCTCCAGTTAAGCTTAACTTCTATCCGTGGAGGAAGCTGTAAAG	6901
Db	6842	ATGAAGCGAAGCGCTCCAGTTAAGCTTAACTTCTATCCGTGGAGGAAGCTGTAAAG	6901
Qy	6902	CTGAGCGCCCCCATTGCGGCCAGATCTAAATTTGGCTATGGGCAAGAGACGTCGGGAAC	6961
Db	6902	CTGAGCGCCCCCATTGCGGCCAGATCTAAATTTGGCTATGGGCAAGAGACGTCGGGAAC	6961

Db	6902	CTGAGCGCCCCCATTGCGGCCAGATCTAAATTTGGCTATGGGCAAGAGACGTCGGGAAC	6961
Qy	6962	CTATCAGCAAGCGCGTTAAACCATCCGCTCCGTGTGGAAGACTTGTCTGGAAGACT	7021
Db	6962	CTATCAGCAAGCGCGTTAAACCATCCGCTCCGTGTGGAAGACTTGTCTGGAAGACT	7021
Qy	7022	GAGACACCAATTTGACACCAACCATCATGGAATAATGAGTTTCTGCGTCCAAACAGAG	7081
Db	7022	GAGACACCAATTTGACACCAACCATCATGGAATAATGAGTTTCTGCGTCCAAACAGAG	7081
Qy	7082	AAGGGGGCGCAAGCCAGCTCGCTTATTCGATTTCCAGATTTGGGGGTTGCTGTGTGC	7141
Db	7082	AAGGGGGCGCAAGCCAGCTCGCTTATTCGATTTCCAGATTTGGGGGTTGCTGTGTGC	7141
Qy	7142	GAGAAAAATGCCCCCTTACGATGTGTCTCCACCCCTCCCTCAGGCCGTGATGGCTTCA	7201
Db	7142	GAGAAAAATGCCCCCTTACGATGTGTCTCCACCCCTCCCTCAGGCCGTGATGGCTTCA	7201
Qy	7202	TACGATTTCCAACTACTCTCTCGACAGCGGTTCGAGTTCCTGTGTAATGCTTGAAGCG	7261
Db	7202	TACGATTTCCAACTACTCTCTCGACAGCGGTTCGAGTTCCTGTGTAATGCTTGAAGCG	7261
Qy	7262	AAGAAATGCCCTTATGGGCTTCGCATATGACACCCGCTGTTTGTGACTCAACGGTCACTGAG	7321
Db	7262	AAGAAATGCCCTTATGGGCTTCGCATATGACACCCGCTGTTTGTGACTCAACGGTCACTGAG	7321
Qy	7322	AATGACATCCGTTGTGAGGAGTCAATCTACCAATGTTGTGACTTGGCCCCCGAGCCAGA	7381
Db	7322	AATGACATCCGTTGTGAGGAGTCAATCTACCAATGTTGTGACTTGGCCCCCGAGCCAGA	7381
Qy	7382	CAGGCCATAAGTTCGCTACAGAGCGGCTTATCATCGGGGGCCCCCTGACTAATTTCTAAA	7441
Db	7382	CAGGCCATAAGTTCGCTACAGAGCGGCTTATCATCGGGGGCCCCCTGACTAATTTCTAAA	7441
Qy	7442	GGGCGAACTGGGGCTATCGCCGTCGCCGCGAGCGGTGTACTGACGACCACTGCGGT	7501
Db	7442	GGGCGAACTGGGGCTATCGCCGTCGCCGCGAGCGGTGTACTGACGACCACTGCGGT	7501
Qy	7502	AATACCTCACAATGTTACTTGAAGCGCTCGGCTGTGAGCTCGGAGCTCCAGGAC	7561
Db	7502	AATACCTCACAATGTTACTTGAAGCGCTCGGCTGTGAGCTCGGAGCTCCAGGAC	7561
Qy	7562	TGCAGCATCTCGTATCGGAGACGACCTTGTGCTTATCTGTAAGAGCGGGGACCCAA	7621
Db	7562	TGCAGCATCTCGTATCGGAGACGACCTTGTGCTTATCTGTAAGAGCGGGGACCCAA	7621
Qy	7622	GAGGACGAGCGGAGCTTACGGGCTTACGGAGGCTATGACTAGATCTCTGCCCCCT	7681
Db	7622	GAGGACGAGCGGAGCTTACGGGCTTACGGAGGCTATGACTAGATCTCTGCCCCCT	7681
Qy	7682	GGGAGCCCCCACCAGAACTACGACTTGGAGTTGATTAACATCATCTCTCAATGTG	7741
Db	7682	GGGAGCCCCCACCAGAACTACGACTTGGAGTTGATTAACATCATCTCTCAATGTG	7741
Qy	7742	TGAGTCGCGCAGATGTCATCTGCAAAAGGTTACTATCTCACCCGTGACCCACACC	7801
Db	7742	TGAGTCGCGCAGATGTCATCTGCAAAAGGTTACTATCTCACCCGTGACCCACACC	7801
Qy	7802	CCCTTTCGCGGGCTGCGTGGGAGACAGCTAGACACTCCAGTCAATTCCTGGCTAGGC	7861
Db	7802	CCCTTTCGCGGGCTGCGTGGGAGACAGCTAGACACTCCAGTCAATTCCTGGCTAGGC	7861
Qy	7862	AACATCATGATGATGCGGCCACTTGTGGGCAAGGATGATCTCTGATGACTCTTCTTC	7921
Db	7862	AACATCATGATGATGCGGCCACTTGTGGGCAAGGATGATCTCTGATGACTCTTCTTC	7921
Qy	7922	TCCATCTTCTAGCTCAGGAAACAACTTGAAAGCCCTAGATTGTGATGATCTACGGGCC	7981
Db	7922	TCCATCTTCTAGCTCAGGAAACAACTTGAAAGCCCTAGATTGTGATGATCTACGGGCC	7981
Qy	7982	TGTTACTTCAATGAGCCACTTGAACCTTACCTCAGATCATTTCAACGACTCCACGCTTAGC	8041
Db	7982	TGTTACTTCAATGAGCCACTTGAACCTTACCTCAGATCATTTCAACGACTCCACGCTTAGC	8041

Db 7982 TGTACTCCATTGAGCCATTGACCTACCTCAGATCAATCAAGCTCCAGCGCCTTAGC 8041  
Qy 8042 GCATTTTCACTCATAGTTACTCTCCAGGTGAGATCAATAGGGTGGCTTCATCCTCAGG 8101  
Db 8042 GCATTTTCACTCATAGTTACTCTCCAGGTGAGATCAATAGGGTGGCTTCATCCTCAGG 8101  
Qy 8102 AAATCTGGGTACCGCCCTTGGAGTCTGGAGATCCGGCCAGAGTGTCCGCGCTAGG 8161  
Db 8102 AAATCTGGGTACCGCCCTTGGAGTCTGGAGATCCGGCCAGAGTGTCCGCGCTAGG 8161  
Qy 8162 CTACTGTCCAGGGGGAGGCTGCGACTTGTGGCAATACCTCTTCAACTGGGAGTA 8221  
Db 8162 CTACTGTCCAGGGGGAGGCTGCGACTTGTGGCAATACCTCTTCAACTGGGAGTA 8221  
Qy 8222 AGACCAAGCTCAAACTCACTCCAAATCCCGGCTGCGTCCAGTTGGATTTATCCAGCTGG 8281  
Db 8222 AGACCAAGCTCAAACTCACTCCAAATCCCGGCTGCGTCCAGTTGGATTTATCCAGCTGG 8281  
Qy 8282 TTCTGTCTGTTACAGCGGGGAGACATATACAGGCTGTCTGTGCGCCGACCCCGC 8341  
Db 8282 TTCTGTCTGTTACAGCGGGGAGACATATACAGGCTGTCTGTGCGCCGACCCCGC 8341  
Qy 8342 TGGTTACGTTGGTCTTACTCTTCTGTAGGGTAGGCATCTATCTACTCTCCCAAC 8401  
Db 8342 TGGTTACGTTGGTCTTACTCTTCTGTAGGGTAGGCATCTATCTACTCTCCCAAC 8401  
Qy 8402 CGATGAACGGGAGCTAAACACTCCAGGCCAATAGGCCATCTGTTTTTCCCTTTTTT 8461  
Db 8402 CGATGAACGGGAGCTAAACACTCCAGGCCAATAGGCCATCTGTTTTTCCCTTTTTT 8461  
Qy 8462 CCCTTT 8521  
Db 8462 CCCTTT 8521  
Qy 8522 TCCCTTT 8581  
Db 8512 TTTCTCTTT 8571  
Qy 8582 GCTGTGAAGGTCGGTAGCGGCTTGACTGACGAGAGTGTGATCTGGCTCTCTGCAG 8641  
Db 8572 GCTGTGAAGGTCGGTAGCGGCTTGACTGACGAGAGTGTGATCTGGCTCTCTGCAG 8631  
Qy 8642 ATCAAGT 8648  
Db 8632 ATCAAGT 8638

RESULT 6  
US-10-789-355-6/c  
; Sequence 6, Application US/10789355  
; GENERAL INFORMATION:  
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.  
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM  
; FILE REFERENCE: 13/083  
; CURRENT APPLICATION NUMBER: US/10/789,355  
; CURRENT FILING DATE: 2004-02-27  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,857  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 8638  
; TYPE: DNA  
; ORGANISM: HCV  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1802)...(8407)  
US-10-789-355-6  
Query Match 0.4%; Score 33.4; DB 1; Length 8638;

Best Local Similarity 49.2%; Pred. No. 0;  
Matches 88; Conservative 0; Mismatches 91; Indels 0; Gaps 0;  
Qy 6120 AGGTAGTAATTTTGGACTCTTTTCGAGCGCTCCAAAGCGGAGGAGTGAAGGAGTAT 6179  
Db 6298 AGGGACGTAGTCCGGGTCCTTCCAGGACTCTAACAGTGGAGGTTTGTAAATCCGGCGTGC 6239  
Qy 6180 CCGTTCCGGCGGAGATCCGCGAGGTCCAGGAAATTCCTCGAGCGATGCCCATATGGG 6239  
Db 6238 CCATATGGGCATCGCTCAGGGAATTTCTTGACCTCCGAGGATCTCCGCGGACGGA 6179  
Qy 6240 CACGCCCGGATTTACAACTTCCACTGTTAGAGTCTCTGGAAGGACCCGGACTACGTCCT 6298  
Db 6178 TACTTCCCTCTCATCTCTCGCTTGGAGCGGCTCGAAAGAGTCCAAAATTAATACCT 6120

RESULT 7  
US-10-789-355-7/c  
; Sequence 7, Application US/10789355  
; GENERAL INFORMATION:  
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.  
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM  
; FILE REFERENCE: 13/083  
; CURRENT APPLICATION NUMBER: US/10/789,355  
; CURRENT FILING DATE: 2004-02-27  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,857  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 8638  
; TYPE: DNA  
; ORGANISM: HCV  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1802)...(8407)  
US-10-789-355-7  
Query Match 0.4%; Score 33.4; DB 1; Length 8638;  
Best Local Similarity 49.2%; Pred. No. 0;  
Matches 88; Conservative 0; Mismatches 91; Indels 0; Gaps 0;  
Qy 6120 AGGTAGTAATTTTGGACTCTTTTCGAGCGCTCCAAAGCGGAGGAGTGAAGGAGTAT 6179  
Db 6298 AGGGACGTAGTCCGGGTCCTTCCAGGACTCTAACAGTGGAGGTTGTAAATCCGGCGTGC 6239  
Qy 6180 CCGTTCCGGCGGAGATCCGCGAGGTCCAGGAAATTCCTCGAGCGATGCCCATATGGG 6239  
Db 6238 CCATATGGGCATCGCTCAGGGAATTTCTTGACCTCCGAGGATCTCCGCGGACGGA 6179  
Qy 6240 CACGCCCGGATTTACAACTTCCACTGTTAGAGTCTCTGGAAGGACCCGGACTACGTCCT 6298  
Db 6178 TACTTCCCTCTCATCTCTCGCTTGGAGCGGCTCGAAAGAGTCCAAAATTAATACCT 6120

RESULT 8  
US-10-789-355-25/c  
; Sequence 25, Application US/10789355  
; GENERAL INFORMATION:  
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.  
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM  
; FILE REFERENCE: 13/083  
; CURRENT APPLICATION NUMBER: US/10/789,355  
; CURRENT FILING DATE: 2004-02-27  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,857  
; NUMBER OF SEQ ID NOS: 25  
US-10-789-355-25  
Query Match 0.4%; Score 33.4; DB 1; Length 8638;

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 25

; LENGTH: 8638

; TYPE: DNA

; ORGANISM: HCV

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1802)...(8407)

US-10-789-355-25

Query Match 0.4%; Score 33.4; DB 1; Length 8638;

Best Local Similarity 49.2%; Pred. No. 0;

Matches 88; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

Qy 6120 AGGTAGTAATTTGGACTCTTTCCGAGCGCTCCAAAGCGGAGGAGATGAGAGGAAGTAT 6179

Db 6298 AGGACGTAGTCGGGTCTTCCAGGACTTAACAGTGGAGGGTTGTAATCCGGCGTGC 6239

Qy 6180 CCGTTCGGCGGAGATCCTCGGAGGTCCAGGAAATTCCTCGAGCGATGCCCATATGGG 6239

Db 6238 CCATATGGCATCGCTCGAGGAATTTCTGGACCTCCGACGATCTCCGCGGAACGGA 6179

Qy 6240 CACGCCGGATTAAACCTCCACTGTAGTCTCGAAGGACCCGGACTACGTCCCT 6298

Db 6178 TACTTCCCTCTCATCTCTCCGCTTGGAGCGGCTCGAAAGAGTCCAAATTTACTACCT 6120

RESULT 9

US-10-789-355-2/c

; Sequence 2, Application US/10789355

; GENERAL INFORMATION:

; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.

; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM

; TITLE OF INVENTION: HEPATITIS C VIRUS

; FILE REFERENCE: 13/083

; CURRENT APPLICATION NUMBER: US/10/789,355

; CURRENT FILING DATE: 2004-02-27

; PRIOR APPLICATION NUMBER: US/10/029,907

; PRIOR FILING DATE: 2001-12-21

; PRIOR APPLICATION NUMBER: 60/257,857

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 8642

; TYPE: DNA

; ORGANISM: HCV

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1802)...(8407)

; FEATURE:

; NAME/KEY: variation

; LOCATION: 6268

; OTHER INFORMATION: r = a or g

; FEATURE:

; NAME/KEY: variation

; LOCATION: 4446

; OTHER INFORMATION: r = a or g

US-10-789-355-2

Query Match

Best Local Similarity 0.4%; Score 33; DB 1; Length 8642;

Matches 87; Conservative 1; Mismatches 91; Indels 0; Gaps 0;

Qy 6120 AGGTAGTAATTTGGACTCTTTCCGAGCGCTCCAAAGCGGAGGAGATGAGAGGAAGTAT 6179

Db 6298 AGGACGTAGTCGGGTCTTCCAGGACTTCYAAAGTGGAGGGTTGTAATCCGGCGTGC 6239

Qy 6180 CCGTTCGGCGGAGATCCTCGGAGGTCCAGGAAATTCCTCGAGCGATGCCCATATGGG 6239

Db 6238 CCATATGGGCATCGCTCGAGGAATTTCTGGACCTCCGACGATCTCCGCGGAACGGA 6179

Qy 6240 CACGCCGGATTAAACCTCTCAGTCTCGAAGGACCCGGACTACGTCCCT 6298

Db 6178 TACTTCCCTCTCATCTCTCCGCTTGGAGCGGCTCGAAAGAGTCCAAATTTACTACCT 6120

RESULT 10

US-10-789-355-4/c

; Sequence 4, Application US/10789355

; GENERAL INFORMATION:

; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.

; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM

; TITLE OF INVENTION: HEPATITIS C VIRUS

; FILE REFERENCE: 13/083

; CURRENT APPLICATION NUMBER: US/10/789,355

; CURRENT FILING DATE: 2004-02-27

; PRIOR APPLICATION NUMBER: US/10/029,907

; PRIOR FILING DATE: 2001-12-21

; PRIOR APPLICATION NUMBER: 60/257,857

; PRIOR FILING DATE: 2000-12-22

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 8643

; TYPE: DNA

; ORGANISM: HCV

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1802)...(8407)

US-10-789-355-4

Query Match 0.4%; Score 31.8; DB 1; Length 8643;

Best Local Similarity 64.0%; Pred. No. 0;

Matches 48; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy 858 CTGGAGCAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCCCGAGGCTCAAGGCGGC 917

Db 932 CTGCGCGTCGGGATGCGGCCCTTGAGCCTGCGGACAGTTGCGTGGCGAGCCCTG 873

Qy 918 ATGCCCCGACGGCGAG 932

Db 872 ATGCTCTTCGTCAG 858

Search completed: March 13, 2007, 16:16:47

Job time : 56 secs



Db 782 ATTTCACCAACGAAACATCGCATCGAGCGACGCTACTCGGATGGAAGCGGTCT 841  
Qy 842 TGTGATCAGGATGATCTGGAAGAGAGATCAGGGGCTCGGCGCAGCGGAATCTTTCG 901  
Db 842 TGTGATCAGGATGATCTGGAAGAGAGATCAGGGGCTCGGCGCAGCGGAATCTTTCG 901  
Qy 902 CAGGCTCAAGGCGCGATCCGCGAGAGAGATCTCGTGTGACCCATGGCGATGCGCTG 961  
Db 902 CAGGCTCAAGGCGCGATCCGCGAGAGATCTCGTGTGACCCATGGCGATGCGCTG 961  
Qy 962 CTTGCGGAATATCATGTGTGAAATAGCGGCTTTTCTGGAATCATCGATGTGGCGGT 1021  
Db 962 CTTGCGGAATATCATGTGTGAAATAGCGGCTTTTCTGGAATCATCGATGTGGCGGT 1021  
Qy 1022 GGGTGTGGCGGACCGGTATCAGGACATAGCGTTGGCTACCGGTGATATGCTGAAGACT 1081  
Db 1022 GGGTGTGGCGGACCGGTATCAGGACATAGCGTTGGCTACCGGTGATATGCTGAAGACT 1081  
Qy 1082 TGGCGGGAATGGGCTGACCGCTTCTCGTGTCTTTACGGTATCGCGCTCCCGATTGCA 1141  
Db 1082 TGGCGGGAATGGGCTGACCGCTTCTCGTGTCTTTACGGTATCGCGCTCCCGATTGCA 1141  
Qy 1142 GGGCATCGGCTTCTATCGCTTCTTGAAGATCTCTGAGTTCTGAGTTCTGCGGCCAGATGTTAA 1201  
Db 1142 GGGCATCGGCTTCTATCGCTTCTTGAAGATCTCTGAGTTCTGAGTTCTGCGGCCAGATGTTAA 1201  
Qy 1202 AGACACAACGGTTTCCCTCTAGCGGATCAATTCGCGCCCCCCCCCTTAAGCTTACTGCG 1261  
Db 1202 AGACACAACGGTTTCCCTCTAGCGGATCAATTCGCGCCCCCCCCCTTAAGCTTACTGCG 1261  
Qy 1262 CGAAGCGGCTTGAATTAAGCGGCTGTGCTTGTCTATATGTTATTTTCCACCATATTG 1321  
Db 1262 CGAAGCGGCTTGAATTAAGCGGCTGTGCTTGTCTATATGTTATTTTCCACCATATTG 1321  
Qy 1322 CCGTCTTTTGGCAATGTGAGGCGCCGGAACCTGGCCCTGTCTTCTGACGAGCATTCCT 1381  
Db 1322 CCGTCTTTTGGCAATGTGAGGCGCCGGAACCTGGCCCTGTCTTCTGACGAGCATTCCT 1381  
Qy 1382 AGGGGTCTTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTAATGTCTGTAAGGAAGCA 1441  
Db 1382 AGGGGTCTTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTAATGTCTGTAAGGAAGCA 1441  
Qy 1442 GTTCTCTCGAAGCTTCTTGAAGACAAACAAAGTCTGAGCGACCTTTGCGAGGAGCGG 1501  
Db 1442 GTTCTCTCGAAGCTTCTTGAAGACAAACAAAGTCTGAGCGACCTTTGCGAGGAGCGG 1501  
Qy 1502 AACCCCCACCTGGCGACAGGTGCTCTGCGGCAAAAGCCACGTGTATPAAGATACACT 1561  
Db 1502 AACCCCCACCTGGCGACAGGTGCTCTGCGGCAAAAGCCACGTGTATPAAGATACACT 1561  
Qy 1562 GCAAGGCGGCAACCCAGTGCCACGTGTGAGTTGGAATAGTATGTAAGATACACT 1621  
Db 1562 GCAAGGCGGCAACCCAGTGCCACGTGTGAGTTGGAATAGTATGTAAGATACACT 1621  
Qy 1622 TGCTCTCTCAAGCTTATCAACAGGCGCTGAAGGATGCCAGAGGTACCCCATTTG 1681  
Db 1622 TGCTCTCTCAAGCTTATCAACAGGCGCTGAAGGATGCCAGAGGTACCCCATTTG 1681  
Qy 1682 ATGGGATCTGATCTGGGGCTCGGTGCAATGCTTTTACATGTGTTTGTGAGGTTAAAA 1741  
Db 1682 ATGGGATCTGATCTGGGGCTCGGTGCAATGCTTTTACATGTGTTTGTGAGGTTAAAA 1741  
Qy 1742 AACGTCTAGCCCCCGCAACCCAGTGCCACGTGTGAGTTGGAATAGTATGTAAGATACACT 1801  
Db 1742 AACGTCTAGCCCCCGCAACCCAGTGCCACGTGTGAGTTGGAATAGTATGTAAGATACACT 1801  
Qy 1802 ATGGACCGGAGATGCGAGCATCGTGGAGGCGGCTTTTCTGAGTCTGATCTTTG 1861  
Db 1802 ATGGACCGGAGATGCGAGCATCGTGGAGGCGGCTTTTCTGAGTCTGATCTTTG 1861  
Qy 1862 ACCTGTGACCGCACTATAGCTGTTCTCGCTAGGCTCATATGTTGGTTTACAAATATTT 1921  
Db 1862 ACCTGTGACCGCACTATAGCTGTTCTCGCTAGGCTCATATGTTGGTTTACAAATATTT 1921

Qy 1922 ATCACCAGGCGGAGGACACACTTTCGAAGTGTGGATCCCCCCTCAACGTTTCGGGGGGC 1981  
Db 1922 ATCACCAGGCGGAGGACACACTTTCGAAGTGTGGATCCCCCCTCAACGTTTCGGGGGGC 1981  
Qy 1982 CGGATGCCGTTCATCTCTCACTCACTGCGGATCCACGAGGTAACTTTTACCATCACC 2041  
Db 1982 CGGATGCCGTTCATCTCTCACTCACTGCGGATCCACGAGGTAACTTTTACCATCACC 2041  
Qy 2042 AAAATCTTGTTCGCGCATACTCGGTCCACTCATGTGTCTCCAGGCTGGTATAAACAAAGTG 2101  
Db 2042 AAAATCTTGTTCGCGCATACTCGGTCCACTCATGTGTCTCCAGGCTGGTATAAACAAAGTG 2101  
Qy 2102 CCGTACTTTCGTCGCGCACACGCGCTCATTCGTGCATGCTGTGTCGGAAGTTGCT 2161  
Db 2102 CCGTACTTTCGTCGCGCACACGCGCTCATTCGTGCATGCTGTGTCGGAAGTTGCT 2161  
Qy 2162 GGGGTCAATATATGTCAAAATGGCTCTCATGAAATGGCTGCGGACGTACGAGTACGTT 2221  
Db 2162 GGGGTCAATATATGTCAAAATGGCTCTCATGAAATGGCTGCGGACGTACGAGTACGTT 2221  
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Db 3842 AGGACTGTGAGGGCAGGATGGGCAATTTACAGTTTGTGACTTCAGGAGAAACGGCCCTCG 3901  
Qy 3902 GGCATGTTTCGATTTCTCGGTTCTGTGCGAGTCTATGACGCGGGTGTCTTGGTACGAG 3961  
Db 3902 GGCATGTTTCGATTTCTCGGTTCTGTGCGAGTCTATGACGCGGGTGTCTTGGTACGAG 3961  
Qy 3962 CTCACGCCCGCGAGACCTCAGTTAGTTGCGGGCTTACCTAAACACACACGAGGTTGCC 4021  
Db 3962 CTCACGCCCGCGAGACCTCAGTTAGTTGCGGGCTTACCTAAACACACACGAGGTTGCC 4021  
Qy 4022 GTCTGCCAGGACCATCTGGAGTTCTGGGAGAGCGCTTTTACAGGCTCACCCACATAGAC 4081  
Db 4022 GTCTGCCAGGACCATCTGGAGTTCTGGGAGAGCGCTTTTACAGGCTCACCCACATAGAC 4081  
Qy 4082 GGGCAATTTCTTGTCTCCAGACTAAGCAGGAGGAGACAACTTCCCTTACCTGGTAGCATAC 4141  
Db 4082 GGGCAATTTCTTGTCTCCAGACTAAGCAGGAGGAGACAACTTCCCTTACCTGGTAGCATAC 4141  
Qy 4142 CAGGCTAGCGGTGCGCCAGGCTCAGGCTCAGCTCCATCTGCTGGGACCAAAATGGAAG 4201  
Db 4142 CAGGCTAGCGGTGCGCCAGGCTCAGGCTCAGCTCCATCTGCTGGGACCAAAATGGAAG 4201  
Qy 4202 TGTCTCATACGGCTAAAGCTACGCTGACGCGGCCAAACGCGCTGCTGTATAGGCTGGGA 4261  
Db 4202 TGTCTCATACGGCTAAAGCTACGCTGACGCGGCCAAACGCGCTGCTGTATAGGCTGGGA 4261  
Qy 4262 GCGGTTCAAAACGAGGTTACTACCAACACACCCCAATAACCAATATCATCATGATGATG 4321  
Db 4262 GCGGTTCAAAACGAGGTTACTACCAACACACCCCAATAACCAATATCATCATGATGATG 4321  
Qy 4322 TCGGCTGACCTGGAGGTGCTGACAGACAGCTGGGTGCTGGTAGGGGAGTCTTAGCAGCT 4381  
Db 4322 TCGGCTGACCTGGAGGTGCTGACAGACAGCTGGGTGCTGGTAGGGGAGTCTTAGCAGCT 4381  
Qy 4382 CTGGCGCGGTATTTGCTGACAAACAGCGAGCTGGTCAATTTGGGCGAGGATCATCTTGTCC 4441  
Db 4382 CTGGCGCGGTATTTGCTGACAAACAGCGAGCTGGTCAATTTGGGCGAGGATCATCTTGTCC 4441  
Qy 4442 GGAAGCGCGGCATCATTTCCCGACAGGGAAGTCTTTTACCGGAGTTTCGATGAGATGGAA 4501  
Db 4442 GGAAGCGCGGCATCATTTCCCGACAGGGAAGTCTTTTACCGGAGTTTCGATGAGATGGAA 4501  
Qy 4502 GAGTGGCGCTCACACTTCCCTTACAGAGGAAATGACAGTCCGCGGAGTCCGCGGATGATCA 4561  
Db 4502 GAGTGGCGCTCACACTTCCCTTACAGAGGAAATGACAGTCCGCGGAGTCCGCGGATGATCA 4561  
Qy 4562 CAGAGGCAATCGGGTGTGCTGCAACAGCACCAAGAGCGGAGGCTGCTGCTCCCGTG 4621  
Db 4562 CAGAGGCAATCGGGTGTGCTGCAACAGCACCAAGAGCGGAGGCTGCTGCTCCCGTG 4621  
Qy 4622 GTGGAATCAAGTGGCGGACCTCGAAGCTTCTGGGCGAAGCATATGTTGGAATTTTCATC 4681  
Db 4622 GTGGAATCAAGTGGCGGACCTCGAAGCTTCTGGGCGAAGCATATGTTGGAATTTTCATC 4681  
Qy 4682 AGCGGATACAAATATTTAGCAGGCTTGTCCACTCTGCTGGGCAACCCCGGATAGCATCA 4741  
Db 4682 AGCGGATACAAATATTTAGCAGGCTTGTCCACTCTGCTGGGCAACCCCGGATAGCATCA 4741  
Qy 4742 CTGATGGCATTCACAGCTCTATCACCGCGCTCACCCACCAACATACCTCTCTGTTT 4801  
Db 4742 CTGATGGCATTCACAGCTCTATCACCGCGCTCACCCACCAACATACCTCTCTGTTT 4801

QY	4802	AACATCTGGGGGATGGGTGGCCGCCCAACTTGTCTCTCCAGCGCTGCTTCTGCTTTC	4861	DB	5882	GTGCTCACTTCATGCTCACCGACCCCTCCACATTAACGGCGAGACGGCTAAGCGTAGG	5941
DB	4802	AACATCTGGGGGATGGGTGGCCGCCCAACTTGTCTCTCCAGCGCTGCTTCTGCTTTC	4861	QY	5942	CTGGCCAGGGATCTCCCCCTCTTGGCCAGCTCATCAGCTAGCCAGCTGTCTCTCGGCC	6001
QY	4862	GTAGGCGCGGCATCGCTGAGCGGCTGTGTGCAGCATAGGCTTGGGAAGGTGCTTGTG	4921	DB	5942	CTGGCCAGGGATCTCCCCCTCTTGGCCAGCTCATCAGCTAGCCAGCTGTCTCTCGGCC	6001
DB	4862	GTAGGCGCGGCATCGCTGAGCGGCTGTGTGCAGCATAGGCTTGGGAAGGTGCTTGTG	4921	QY	6002	TCCTTGAAGGCAACATGCACTACCCGTCATGACTCCCCCGGACGCTGACTCATCGAGGCC	6061
QY	4922	GATATTTTGGCAGGTTATGGACAGGGGTGGACGGCGGCTCGTGGCCCTTAAAGTCAAG	4981	DB	6002	TCCTTGAAGGCAACATGCACTACCCGTCATGACTCCCCCGGACGCTGACTCATCGAGGCC	6061
DB	4922	GATATTTTGGCAGGTTATGGACAGGGGTGGACGGCGGCTCGTGGCCCTTAAAGTCAAG	4981	QY	6062	AACCTCTGTGGCGGAGGAGATGGGCGGGAACATACACCCGGTGGAGTCAAGAAATAAG	6121
QY	4982	AGCGGAGATGCTCCACCGAGGACCTGGTTAACTACTCTCTCTATCTCTCTCTCTCT	5041	DB	6062	AACCTCTGTGGCGGAGGAGATGGGCGGGAACATACACCCGGTGGAGTCAAGAAATAAG	6121
DB	4982	AGCGGAGATGCTCCACCGAGGACCTGGTTAACTACTCTCTCTATCTCTCTCTCTCT	5041	QY	6122	GTAGTAAATTTTGGACTCTTTTCGAGCGCTCCAAAGCGGAGGAGATGAGAGGGAATATTC	6181
QY	5042	GGCGCCCTAGTCTCGGGGTGCTGTGCGCAGCGATATCTGCTGCGCACTGCTGGGCCAGGG	5101	DB	6122	GTAGTAAATTTTGGACTCTTTTCGAGCGCTCCAAAGCGGAGGAGATGAGAGGGAATATTC	6181
DB	5042	GGCGCCCTAGTCTCGGGGTGCTGTGCGCAGCGATATCTGCTGCGCACTGCTGGGCCAGGG	5101	QY	6182	GTTCGGCGGAGATCTTCGCGGAGGTCCAGGAAATTCCTCGAGCGATGCCATATGGGCA	6241
QY	5102	GAGGGGCTGTGAGTGGATGAACCGGCTGATAGCGTTGCTTCGCGGGGTAAACCACTGC	5161	DB	6182	GTTCGGCGGAGATCTTCGCGGAGGTCCAGGAAATTCCTCGAGCGATGCCATATGGGCA	6241
DB	5102	GAGGGGCTGTGAGTGGATGAACCGGCTGATAGCGTTGCTTCGCGGGGTAAACCACTGC	5161	QY	6242	CGCCCGGATTAAACCCCTCCACTGTAGATCTTGGAAGGACCCCGGACTACGTCCTCCA	6301
QY	5162	TCCCCACGCACTATGCTGCTGAGAGCGCTGCAGCAGTGTCACTCAGATCTCTCTCT	5221	DB	6242	CGCCCGGATTAAACCCCTCCACTGTAGATCTTGGAAGGACCCCGGACTACGTCCTCCA	6301
DB	5162	TCCCCACGCACTATGCTGCTGAGAGCGCTGCAGCAGTGTCACTCAGATCTCTCTCT	5221	QY	6302	GTGGTACACGGGTGTCATTCGCCGCTCCAAAGGCCCCCTCGATACCACTCCACGGAGG	6361
QY	5222	AGTCTTACCATCACTCAGCTGCTGGAAGAGGCTTACCAGTGGATCAACGAGGACTGCTCC	5281	DB	6302	GTGGTACACGGGTGTCATTCGCCGCTCCAAAGGCCCCCTCGATACCACTCCACGGAGG	6361
DB	5222	AGTCTTACCATCACTCAGCTGCTGGAAGAGGCTTACCAGTGGATCAACGAGGACTGCTCC	5281	QY	6362	AAGAGGACGGTGTCTCTCAGAAATCTACCGTGTCTTCTGCTTGGCGGAGCTCCGCA	6421
QY	5282	ACGCCATGCTCGGCTGCTGCTGGAAGAGGCTTACCAGTGGATCAACGAGGACTGCTCC	5341	DB	6362	AAGAGGACGGTGTCTCTCAGAAATCTACCGTGTCTTCTGCTTGGCGGAGCTCCGCA	6421
DB	5282	ACGCCATGCTCGGCTGCTGCTGGAAGAGGCTTACCAGTGGATCAACGAGGACTGCTCC	5341	QY	6422	AAGACCTTGGCAGCTCCGAATCTGTCGGCGTGCAGGGGACCGGCAACGGCCCTCTCT	6481
QY	5342	GATTTCAAGACCTGGCTCCAGTCCAAAGCTCTCCCGCGATTGCGGGAGTCCCTCTTTC	5401	DB	6422	AAGACCTTGGCAGCTCCGAATCTGTCGGCGTGCAGGGGACCGGCAACGGCCCTCTCT	6481
DB	5342	GATTTCAAGACCTGGCTCCAGTCCAAAGCTCTCCCGCGATTGCGGGAGTCCCTCTTTC	5401	QY	6482	GACCAACCTCCGACGAGCGGACCGCGGATCCGACGTTGAGTCTGCTCTCCATGGCCC	6541
QY	5402	TCATGTCAACGCTGGGTACAGGAGGCTGTGGCGGGGCGAGCGCATATGCAAAACCACTGC	5461	DB	6482	GACCAACCTCCGACGAGCGGACCGCGGATCCGACGTTGAGTCTGCTCTCCATGGCCC	6541
DB	5402	TCATGTCAACGCTGGGTACAGGAGGCTGTGGCGGGGCGAGCGCATATGCAAAACCACTGC	5461	QY	6542	CCCTTTGAGGGGAGCCCGGGGATCCCGATCTCAGGACGGGCCCTTGGTCTACCGTAAGC	6601
QY	5462	CCATGTGGAGCA CAGATACACCGGACATGTGAAAAAATGTTTCCATGAGGATCGTGGGCT	5521	DB	6542	CCCTTTGAGGGGAGCCCGGGGATCCCGATCTCAGGACGGGCCCTTGGTCTACCGTAAGC	6601
DB	5462	CCATGTGGAGCA CAGATACACCGGACATGTGAAAAAATGTTTCCATGAGGATCGTGGGCT	5521	QY	6602	GAGGAGGCTAGTGAGGACGTCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	6661
QY	5522	AGGACCTGTAGTAACACGCTGGCATGGAACATTCCTCCATTAACCGCTACACCGGGCCCC	5581	DB	6602	GAGGAGGCTAGTGAGGACGTCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	6661
DB	5522	AGGACCTGTAGTAACACGCTGGCATGGAACATTCCTCCATTAACCGCTACACCGGGCCCC	5581	QY	6662	ATCAGCCATGCGCTGGGAGGAAACCAAGCTGCCCATCAATGCACTGAGCAACTCTTTTG	6721
QY	5582	TGCACGCGCTCCCGCGCGCAAAATTTCTAGGGCGCTGTGGCGGGTGGCTGTGAGGAG	5641	DB	6662	ATCAGCCATGCGCTGGGAGGAAACCAAGCTGCCCATCAATGCACTGAGCAACTCTTTTG	6721
DB	5582	TGCACGCGCTCCCGCGCGCAAAATTTCTAGGGCGCTGTGGCGGGTGGCTGTGAGGAG	5641	QY	6722	CTCCGTACCAACACTTGGTCTATGCTACAAATCTCGCAGCGCAAGCTTGGGCAAG	6781
QY	5642	TACGTGGAGGTTACGCGGTGGGGATTTTCCATGTCGAGCGGATGACCACTGACAAAC	5701	DB	6722	CTCCGTACCAACACTTGGTCTATGCTACAAATCTCGCAGCGCAAGCTTGGGCAAG	6781
DB	5642	TACGTGGAGGTTACGCGGTGGGGATTTTCCATGTCGAGCGGATGACCACTGACAAAC	5701	QY	6782	AAGGTCAACCTTTGACAGACTGCGAGTCTGGAAGCACTACCGGAGCGTGTCAAGGAG	6841
QY	5702	GTAAAGTGGCGGTGTGAGTTTCGGGCCCCCGAATTTCTTACAGAGTGGATGGGTGCGG	5761	DB	6782	AAGGTCAACCTTTGACAGACTGCGAGTCTGGAAGCACTACCGGAGCGTGTCAAGGAG	6841
DB	5702	GTAAAGTGGCGGTGTGAGTTTCGGGCCCCCGAATTTCTTACAGAGTGGATGGGTGCGG	5761	QY	6842	ATGAAGGCGAAGGCTGCACAGTTAAGGCTAACTTCTATCCGTGGAGGAGGCTCTAAG	6901
QY	5762	TTGCACAGGTACGCTCCAGCGTGCABACCCCTCTACGAGGAGGAGTCAATTCCTGGTC	5821	DB	6842	ATGAAGGCGAAGGCTGCACAGTTAAGGCTAACTTCTATCCGTGGAGGAGGCTCTAAG	6901
DB	5762	TTGCACAGGTACGCTCCAGCGTGCABACCCCTCTACGAGGAGGAGTCAATTCCTGGTC	5821	QY	6902	CTGAGCGCCCCACATTCGCGCCAGATCTAAATTTGGCTATGGGCAAGGACGTCGCGAAC	6961
QY	5822	GGGCTCAATCAATACCTGGTGGGTACAGCTCCCATGCGAGGCCCGAACCAGGAGTAGCA	5881	DB	6902	CTGAGCGCCCCACATTCGCGCCAGATCTAAATTTGGCTATGGGCAAGGACGTCGCGAAC	6961
DB	5822	GGGCTCAATCAATACCTGGTGGGTACAGCTCCCATGCGAGGCCCGAACCAGGAGTAGCA	5881	QY	6962	CTATCCAGCAAGGCGCTTAAACCACTCCGCTCCGTGTGGAGGAGCTTGTGGAAGACACT	7021
QY	5882	GTGCTCACTTCCATGCTCAACGACCCCTCCCACTTAACGGGAGAGCGGCTAAGCGTAGG	5941				

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Db      6962  CTATCAGCAAGGCCGTTAAACACATCCGCTCCGTGCGAAGGACTTGCTGGAAGACACT 7021
Qy      7022  GAGACACCAATTGACACACCATCATGCGCAAAATAGAGTTTCTGCGCTCCAAACGAG 7081
Db      7022  GAGACACCAATTGACACACCATCATGCGCAAAATAGAGTTTCTGCGCTCCAAACGAG 7081
Qy      7082  AAGGGGGGGCGCAAGCGAGCTCGCCCTTATCGTATCCAGATTTGGGGGTTCTGTGTGC 7141
Db      7082  AAGGGGGGGCGCAAGCGAGCTCGCCCTTATCGTATCCAGATTTGGGGGTTCTGTGTGC 7141
Qy      7142  GAGAAATGGCCCTTTACGATGFGTCTCCACCTCCCTCAGCCGTGATGGGCTCTTCA 7201
Db      7142  GAGAAATGGCCCTTTACGATGFGTCTCCACCTCCCTCAGCCGTGATGGGCTCTTCA 7201
Qy      7202  TACGGATTCATACACTCTCTCGACAGCGGTTCGAGTTCTCGTGAATGCTTGGAAAGG 7261
Db      7202  TACGGATTCATACACTCTCTCGACAGCGGTTCGAGTTCTCGTGAATGCTTGGAAAGG 7261
Qy      7262  AAGAAATGGCCCTATGGGCTTCGATATGACACCGCTGTTTGTACTCAACGGTCACTGAG 7321
Db      7262  AAGAAATGGCCCTATGGGCTTCGATATGACACCGCTGTTTGTACTCAACGGTCACTGAG 7321
Qy      7322  AATGACATCCGTTTGAAGGCTCAATCTACCAATGTTGACTTGGCCCCCGAAGCCAGA 7381
Db      7322  AATGACATCCGTTTGAAGGCTCAATCTACCAATGTTGACTTGGCCCCCGAAGCCAGA 7381
Qy      7382  CAGGCCATGAGTCTGCTCAGAGCGGCTTACATCGGGGGCCCCCTGACTAATTTCTAAA 7441
Db      7382  CAGGCCATGAGTCTGCTCAGAGCGGCTTACATCGGGGGCCCCCTGACTAATTTCTAAA 7441
Qy      7442  GGGCAGAACTGGGCTATCCGGTCCCGCGAGCGGTGTACTGACGACACGAGTGGCGT 7501
Db      7442  GGGCAGAACTGGGCTATCCGGTCCCGCGAGCGGTGTACTGACGACACGAGTGGCGT 7501
Qy      7502  AATACCTCCATGTTACTTGAAGCGCGTTCGGGCTGTGAGCTGCGAAGCTCCAGGAC 7561
Db      7502  AATACCTCCATGTTACTTGAAGCGCGTTCGGGCTGTGAGCTGCGAAGCTCCAGGAC 7561
Qy      7562  TGCAGATCTCGTATGCGGACGACCTTGTGTTATCTGTGAAAGCGGGGGACCCAA 7621
Db      7562  TGCAGATCTCGTATGCGGACGACCTTGTGTTATCTGTGAAAGCGGGGGACCCAA 7621
Qy      7622  GAGGACGAGCGAGCTTACGGGCTTACGAGGCTATGACTAGATCTCTGCCGCCCT 7681
Db      7622  GAGGACGAGCGAGCTTACGGGCTTACGAGGCTATGACTAGATCTCTGCCGCCCT 7681
Qy      7682  GGGACCCCGCCAAACAGAAATACGACTTGGAGTTGATAAATCAATCTCTCCAAATG 7741
Db      7682  GGGACCCCGCCAAACAGAAATACGACTTGGAGTTGATAAATCAATCTCTCCAAATG 7741
Qy      7742  TCAGTCGCGACGATGCTGCGCAAAAGGTTGACTATCTACCCGTGACCCGACCCAGC 7801
Db      7742  TCAGTCGCGACGATGCTGCGCAAAAGGTTGACTATCTACCCGTGACCCGACCCAGC 7801
Qy      7802  CCCCTTGGCGGCTCGGTGGGAGACAGCTAGACACACTCCAGTCAATCTCTGGCTAGC 7861
Db      7802  CCCCTTGGCGGCTCGGTGGGAGACAGCTAGACACACTCCAGTCAATCTCTGGCTAGC 7861
Qy      7862  AACATCATCATGTATGCGGCCACTTTGTGGCAAGGATGATCTGATGACTCATTTCTTC 7921
Db      7862  AACATCATCATGTATGCGGCCACTTTGTGGCAAGGATGATCTGATGACTCATTTCTTC 7921
Qy      7922  TCATCTCTTCTAGCTCAGGAACCACTTGAAAGCCCTAGATTCAGATCTACGGGGCC 7981
Db      7922  TCATCTCTTCTAGCTCAGGAACCACTTGAAAGCCCTAGATTCAGATCTACGGGGCC 7981
Qy      7982  TGTACTCTTCTAGCTCAGGAACCACTTACCTTACATCTTCAAGCATCTCAGGCGCTTAC 8041
Db      7982  TGTACTCTTCTAGCTCAGGAACCACTTACCTTACATCTTCAAGCATCTCAGGCGCTTAC 8041
Qy      8042  GCATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGTTGCTTCTATGCTCAG 8101
Db      8042  GCATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGTTGCTTCTATGCTCAG 8101
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Qy      8102  AAATTGGGGTACCGCCCTTCGGAGTCTGGAGACATCGGGCCAGAGTGTCCGCGCTAGG 8161
Db      8102  AAATTGGGGTACCGCCCTTCGGAGTCTGGAGACATCGGGCCAGAGTGTCCGCGCTAGG 8161
Qy      8162  CTACTGTCCAGGGGGGAGGGCTGCCACTTGTGGCAAGTACCTCTTCAACTGGGCACTA 8221
Db      8162  CTACTGTCCAGGGGGGAGGGCTGCCACTTGTGGCAAGTACCTCTTCAACTGGGCACTA 8221
Qy      8222  AGGACCAAGCTCAAACTCACTCCCAATCCCGGCTGGGTCCAGTTGGATTTATCCAGCTGG 8281
Db      8222  AGGACCAAGCTCAAACTCACTCCCAATCCCGGCTGGGTCCAGTTGGATTTATCCAGCTGG 8281
Qy      8282  TTGTTGCTGCTTACAGCGGGGAGACATATATCACGCCCTGTCTCGTGCCCGACCCCGC 8341
Db      8282  TTGTTGCTGCTTACAGCGGGGAGACATATATCACGCCCTGTCTCGTGCCCGACCCCGC 8341
Qy      8342  TGGTTACGTTGCTACTCTCTACTTCTGAGGGTAGGCATCTATCTACTCTCCCAAC 8401
Db      8342  TGGTTACGTTGCTACTCTCTACTTCTGAGGGTAGGCATCTATCTACTCTCCCAAC 8401
Qy      8402  CGATGAACGGGAGCTAAACACTCCAGGCCAATAGGCCATCTCTGTTTCTCCCTTTT 8461
Db      8402  CGATGAACGGGAGCTAAACACTCCAGGCCAATAGGCCATCTCTGTTTCTCCCTTTT 8461
Qy      8462  CCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 8521
Db      8462  TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 8511
Qy      8522  TCCCTTTTTTTTTTTCTTTCTTTTCTTTTGGTGGCTCCATCTTAGCCCTAGTCAGGCTA 8581
Db      8512  TTCTCTTTTTTTTTTCTTTCTTTTCTTTTGGTGGCTCCATCTTAGCCCTAGTCAGGCTA 8571
Qy      8582  GCTGTGAAAGTCCGTGAGCGCTTGACTGACAGAGTGTGATGATGCTGCTCTGTCAG 8641
Db      8572  GCTGTGAAAGTCCGTGAGCGCTTGACTGACAGAGTGTGATGATGCTGCTCTGTCAG 8631
Qy      8642  ATCAAGT 8648
Db      8632  ATCAAGT 8638
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## RESULT 3

US-10-789-355-4

; Sequence 4, Application US/10789355

; GENERAL INFORMATION:

; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.

; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM

; TITLE OF INVENTION: HEPATITIS C VIRUS

; FILE REFERENCE: 13/083

; CURRENT APPLICATION NUMBER: US/10/789,355

; CURRENT FILING DATE: 2004-02-27

; PRIOR APPLICATION NUMBER: US/10/029,907

; PRIOR FILING DATE: 2001-12-21

; PRIOR APPLICATION NUMBER: 60/257,857

; PRIOR FILING DATE: 2000-12-22

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 8643

; TYPE: DNA

; ORGANISM: HCV

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1802)...(8407)

US-10-789-355-4

Query Match

Best Local Similarity 99.3%; Score 8584.7; DB 1; Length 8643;

Matches 8614; Conservative 0; Mismatches 28; Indels 5; Gaps 1;

Qy 2 CCAGCCCCCGATTGGGGCGGACACTCCACCATAGATCACTCCCTGTGAGGAATCTGT 61



Db 2 CCAGCCCCCGATTGGGGCGCACTCCACCATAGATCACTCCCTGTGAGGAATCTACTGT 61  
Qy 62 CTTTCACGCAAGAGCGTCTAGCCATGGCGTTAGTATGAGTGTCTGTCAGCCCTCCAGGACC 121  
Db 62 CTTTCACGCAAGAGCGTCTAGCCATGGCGTTAGTATGAGTGTCTGTCAGCCCTCCAGGACC 121  
Qy 122 CCCCTCCCGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATTCGCCAGG 181  
Db 122 CCCCTCCCGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATTCGCCAGG 181  
Qy 182 ACGACCGGTCCTTTCTTGGATCAACCCCGCTCAATGCTCTGAGATTTGGCGGTGCCCCCG 241  
Db 182 ACGACCGGTCCTTTCTTGGATCAACCCCGCTCAATGCTCTGAGATTTGGCGGTGCCCCCG 241  
Qy 242 CGAGACTGTAGCCGAGTGTGTGGTTCGGAAGGCGCTTGTGTACTGTGCTGATAGGG 301  
Db 242 CGAGACTGTAGCCGAGTGTGTGGTTCGGAAGGCGCTTGTGTACTGTGCTGATAGGG 301  
Qy 302 TGTCTTGGAGTGCCTGGGAGGTCTGTAAGCCGTGCACCATGAGCAGGAATCCTAAACC 361  
Db 302 TGTCTTGGAGTGCCTGGGAGGTCTGTAAGCCGTGCACCATGAGCAGGAATCCTAAACC 361  
Qy 362 TCAAGAAAAAACAAGGCGCGCATGATTGAACAAGATGATTCACGCAAGTTCTCC 421  
Db 362 TCAAGAAAAAACAAGGCGCGCATGATTGAACAAGATGATTCACGCAAGTTCTCC 421  
Qy 422 GCGCGTTGGGTGGAGAGGCTATTGGCTATGACTGGGCAACAAGACATCGGCTGCTC 481  
Db 422 GCGCGTTGGGTGGAGAGGCTATTGGCTATGACTGGGCAACAAGACATCGGCTGCTC 481  
Qy 482 TGAATGCGCGGTTCCTGGGCTGTGACGCGAGGGCGCCGGTCTTTTGTCAAGACCGA 541  
Db 482 TGAATGCGCGGTTCCTGGGCTGTGACGCGAGGGCGCCGGTCTTTTGTCAAGACCGA 541  
Qy 542 CTTGTCGGTGCCTGAAATGAATCTGAGCAGGAGCGCGGCTATCGTGGCTGGCCAC 601  
Db 542 CTTGTCGGTGCCTGAAATGAATCTGAGCAGGAGCGCGGCTATCGTGGCTGGCCAC 601  
Qy 602 GACGGCGTTCCTTGGCGAGTGTGTGCTGACGTTGTCACTGAAGCGGGAGGAGTGGCT 661  
Db 602 GACGGCGTTCCTTGGCGAGTGTGTGCTGACGTTGTCACTGAAGCGGGAGGAGTGGCT 661  
Qy 662 GCTATTGGGCGAAGTCCGGGCGAGATCTCTGTGATCTCACTTGTCTCTGCGGAGAA 721  
Db 662 GCTATTGGGCGAAGTCCGGGCGAGATCTCTGTGATCTCACTTGTCTCTGCGGAGAA 721  
Qy 722 AGTATCCATCATGGCTGATGCAATGCGGGGTGCACTAGCTTTGATCCGGCTACCTGCC 781  
Db 722 AGTATCCATCATGGCTGATGCAATGCGGGGTGCACTAGCTTTGATCCGGCTACCTGCC 781  
Qy 782 ATTTCGACCAAGCGAAACATCGCATTCGAGCGAGCACGTACTCGGATGGAGCGGGTCT 841  
Db 782 ATTTCGACCAAGCGAAACATCGCATTCGAGCGAGCACGTACTCGGATGGAGCGGGTCT 841  
Qy 842 TGTGATCAGGATGATCTGGACGAAGCATCAGGGGCTCGCGCCAGCGCACTGTTGCG 901  
Db 842 TGTGATCAGGATGATCTGGACGAAGCATCAGGGGCTCGCGCCAGCGCACTGTTGCG 901  
Qy 902 CAGGCTCAAGCGCGCATGCCGACGCGAGGATCTCGTGTGACCCCATGGGATGCGCTG 961  
Db 902 CAGGCTCAAGCGCGCATGCCGACGCGAGGATCTCGTGTGACCCCATGGGATGCGCTG 961  
Qy 962 CTTTGGCGAATATCATGGTGGAAAAATGGCGCTTTTCTGGAATTCATCGATGTGGCGGGCT 1021  
Db 962 CTTTGGCGAATATCATGGTGGAAAAATGGCGCTTTTCTGGAATTCATCGATGTGGCGGGCT 1021  
Qy 1022 GGTGTGGCGGACCGCTATCAGACATAGCGTTGGCTACCCGTGATATTCCTGGAAGCT 1081  
Db 1022 GGTGTGGCGGACCGCTATCAGACATAGCGTTGGCTACCCGTGATATTCCTGGAAGCT 1081  
Qy 1082 TGGCGGGAATGGGCTGACCGCTTCTCTGCTTTTACGGTATCGCGCTCCCGATTTCGA 1141  
Db 1082 TGGCGGGAATGGGCTGACCGCTTCTCTGCTTTTACGGTATCGCGCTCCCGATTTCGA 1141

Qy 1142 GGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGTTTCGCGCCAGATGTTAAC 1201  
Db 1142 GGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGTTTCGCGCCAGATGTTAAC 1201  
Qy 1202 AGACCAACAAAGGTTTCCCTCTAGCGGATCAATTCGCGCCCGCCCTTAACGTTACTGGC 1261  
Db 1202 AGACCAACAAAGGTTTCCCTCTAGCGGATCAATTCGCGCCCGCCCTTAACGTTACTGGC 1261  
Qy 1262 CGAAGCGCTTGGAAATAGGCGCGTGTGCTTGTCTATATGTTATTTTCCACCATATG 1321  
Db 1262 CGAAGCGCTTGGAAATAGGCGCGTGTGCTTGTCTATATGTTATTTTCCACCATATG 1321  
Qy 1322 CCGTCTTTTGGCAATGTAGGGCCCGGAAACCTGGCCCTGTCTTCTTGACGAGCATTCCT 1381  
Db 1322 CCGTCTTTTGGCAATGTAGGGCCCGGAAACCTGGCCCTGTCTTCTTGACGAGCATTCCT 1381  
Qy 1382 AGGGGTCTTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTGAAATGCTGAGGAAGCA 1441  
Db 1382 AGGGGTCTTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTGAAATGCTGAGGAAGCA 1441  
Qy 1442 GTTCTCTGGAAGCTTCTTGAAGCAAAACACGTCGTAGCGACCTTTGCGAGCAGCG 1501  
Db 1442 GTTCTCTGGAAGCTTCTTGAAGCAAAACACGTCGTAGCGACCTTTGCGAGCAGCG 1501  
Qy 1502 AACCCCGACCTGCGACAGGTCTCTGCGCCAAAGGACACGCTGTATAAGATACACCT 1561  
Db 1502 AACCCCGACCTGCGACAGGTCTCTGCGCCAAAGGACACGCTGTATAAGATACACCT 1561  
Qy 1562 GCAAAGGCGGCAACCCAGTGCACGTTGTGAGTTGGATGAGTTGCGAAGAGTCAAA 1621  
Db 1562 GCAAAGGCGGCAACCCAGTGCACGTTGTGAGTTGGATGAGTTGCGAAGAGTCAAA 1621  
Qy 1622 TGGCTCTCTCAGGATTTCAAAGGGCTGAGGATGCCAGAGGTACCCCATTTGT 1681  
Db 1622 TGGCTCTCTCAGGATTTCAAAGGGCTGAGGATGCCAGAGGTACCCCATTTGT 1681  
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Db 1922 ATCACAGGCGCGAGGCACTTGCAGTGTGGATTCGCCCTCAAGCTTCGGGGGGG 1981  
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Db 2102 CCGTACTTCTGTCGCGCAACGCGGCTCATTCGTGATGCTGCTGGTGGAGGTTGCT 2161  
Qy 2162 GGGGTCTATTATGTCGCGCAACGCGGCTCATTCGTGATGCTGCTGGTGGAGGTTGCT 2221  
Db 2162 GGGGTCTATTATGTCGCGCAACGCGGCTCATTCGTGATGCTGCTGGTGGAGGTTGCT 2221



QY 2222 TATGACCATCTCACCCACCTGCGGACTGGGCCCAACGCGGGCCTACGAGACCTTTCGGGTG 2281  
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QY 4382 CTGGCGCGTATTTGCTGTGACAAACAGGACGCTGCTATTTGTGGGAGGATCATCTTGTGCC 4441

Db	4382	CTGGCGCGTATTGCTGACACAGCAGCGGTGGTCAATTGTGGCAGGATCATCTTGTC	4441	Qy	5522	AGGACCTCTAGTAAACAGTGGCATGGAAACATTCCCAATTAAACGGGTACACACAGGGCCCC	5581
Qy	4442	GGAAAGCCGGCCATCATTTCCCGACAGGGAAGTCTTTTACCGGAGTTTGATGAGATGGAA	4501	Db	5522	AGGACCTGTAGTAACACGTGGCATGGAAACATTCCCAATTAAACGGGTACACACAGGGCCCC	5581
Db	4442	GGAAAGCCGGCCATCATTTCCCGACAGGGAAGTCTTTTACCGGAGTTTGATGAGATGGAA	4501	Qy	5582	TGCACGGCCCTCCCGGGGCCAAATTTATTTCTAGGGCGCTGTGGCGGGTGGCTGCTGAGGAG	5641
Qy	4502	GAGTGGCCTCACACCTCCCTTACATCGAACAGGGAATCAGCTCGCGAAACAAATTCAAA	4561	Db	5582	TGCACGGCCCTCCCGGGGCCAAATTTATTTCTAGGGCGCTGTGGCGGGTGGCTGCTGAGGAG	5641
Db	4502	GAGTGGCCTCACACCTCCCTTACATCGAACAGGGAATCAGCTCGCGAAACAAATTCAAA	4561	Qy	5642	TACGTGAGGTTACGCGGTGGGGATTTTCACTACGTGACGGGCATGACCACTGACAC	5701
Qy	4562	CAGAGGCAATCGGTTGTGCAAAACAGCCACCAAGCAAGCGAGGCTGCTCCCGTG	4621	Db	5642	TACGTGAGGTTACGCGAGTGGGGATTTTCACTACGTGACGGGCATGACCACTGACAC	5701
Db	4562	CAGAGGCAATCGGTTGTGCAAAACAGCCACCAAGCAAGCGAGGCTGCTCCCGTG	4621	Qy	5702	GTAAGTGCCTGTGTCAGTTCCCGCCCCCGAAATTTCTTCAAGAGTGGATGGGTGGG	5761
Qy	4622	GTGGAATCCAAGTGGCGGACCTTCGAAGCTTTCTGGCGAAGCATATGTGGAATTTTCATC	4681	Db	5702	GTAAGTGCCTGTGTCAGTTCCCGCCCCCGAAATTTCTTCAAGAGTGGATGGGTGGG	5761
Db	4622	GTGGAATCCAAGTGGCGGACCTTCGAAGCTTTCTGGCGAAGCATATGTGGAATTTTCATC	4681	Qy	5762	TTGCACAGGTACGTTCACAGCGTGCACACCCCTCTCTAGCGGAGGAGTCACTTCCTGTGC	5821
Qy	4682	AGCGGATACAAATATTTAGAGGCTTTGTCCACTCTGCCCTGGCAACCCCGCGATAGCATCA	4741	Db	5762	TTGCACAGGTACGTTCACAGCGTGCACACCCCTCTCTAGCGGAGGAGTCACTTCCTGTGC	5821
Db	4682	AGCGGATACAAATATTTAGAGGCTTTGTCCACTCTGCCCTGGCAACCCCGCGATAGCATCA	4741	Qy	5822	GGGCTCAATCAATACCTGGTGGGTACAGTCCCATGCGAGGCCGCAACCGGACGTAGCA	5881
Qy	4742	CTGATGGCATTCACAGCTCTATACACAGCCGCTCACACCCGCTCACACCCCTCTCTGTTT	4801	Db	5822	GGGCTCAATCAATACCTGGTGGGTACAGTCCCATGCGAGGCCGCAACCGGACGTAGCA	5881
Db	4742	CTGATGGCATTCACAGCTCTATACACAGCCGCTCACACCCGCTCACACCCCTCTCTGTTT	4801	Qy	5882	GTGCTCACTTCCATGCTCACCAGCCCTCCACATTCACGGCGGAGACGGCTAAGCGTAGG	5941
Qy	4802	AACATCCTGGGGGATGGGTGGCGGCCAACTTGTCTCTCCAGCGCTGCTTCTGTTTC	4861	Db	5882	GTGCTCACTTCCATGCTCACCAGCCCTCCACATTCACGGCGGAGACGGCTAAGCGTAGG	5941
Db	4802	AACATCCTGGGGGATGGGTGGCGGCCAACTTGTCTCTCCAGCGCTGCTTCTGTTTC	4861	Qy	5942	CTGSCAGGGGATCTCCCGCTCTTGGCCAGCTCATCAGCTAGCCAGCTGCTCTCGGCC	6001
Qy	4862	GTAGGCGCGGATCGCTCGAGCGGCTGTGCGAGCATAGGCTTGGGAAGTGTCTTG	4921	Db	5942	CTGSCAGGGGATCTCCCGCTCTTGGCCAGCTCATCAGCTAGCCAGCTGCTCTCGGCC	6001
Db	4862	GTAGGCGCGGATCGCTCGAGCGGCTGTGCGAGCATAGGCTTGGGAAGTGTCTTG	4921	Qy	6002	TCCTTGAAGGCAACATGCACTACCGTCTATGACTCCCGGACGCTGACTCATCGAGCC	6061
Qy	4922	GATATTTTGGCAGTTATGAGCAGGGGTGGCAGCGCTGCTGGGCCCTTTAAGGTTCATG	4981	Db	6002	TCCTTGAAGGCAACATGCACTACCGTCTATGACTCCCGGACGCTGACTCATCGAGCC	6061
Db	4922	GATATTTTGGCAGTTATGAGCAGGGGTGGCAGCGCTGCTGGGCCCTTTAAGGTTCATG	4981	Qy	6062	AACCTCTGTGCGGACAGAGATGGCGGGAACATCAACCGGTGGAGTCAGAAATAAG	6121
Qy	4982	AGCGGAGATGCGCTTCCACCGAGACCTGGTTAACTTACTCCCTGCTATCTCTCCCT	5041	Db	6062	AACCTCTGTGCGGACAGAGATGGCGGGAACATCAACCGGTGGAGTCAGAAATAAG	6121
Db	4982	AGCGGAGATGCGCTTCCACCGAGACCTGGTTAACTTACTCCCTGCTATCTCTCCCT	5041	Qy	6122	GTAGTAATTTTGGACTCTTTTGGAGCTCTTTCGAGCGCTTCCAGCGGAGGAGATGAGAGGAAATATCC	6181
Qy	5042	GGCGCCCTAGTCTGCGGGTCTGTCGAGCGATCTGCTGCGGACGCTGCGGCCCGCAGG	5101	Db	6122	GTAGTAATTTTGGACTCTTTTGGAGCTCTTTCGAGCGCTTCCAGCGGAGGAGATGAGAGGAAATATCC	6181
Db	5042	GGCGCCCTAGTCTGCGGGTCTGTCGAGCGATCTGCTGCGGACGCTGCGGCCCGCAGG	5101	Qy	6182	GTTCGGCGGAGATCTTCGAGGAGTCCAGGAAATTTCCCTCGAGCGATGCCCATATGGGCA	6241
Qy	5102	GAGGGGCTGTGAGTGGATGAACCGGCTGATAGCGTTCCGTTCCGCGGGTAAACACGTC	5161	Db	6182	GTTCGGCGGAGATCTTCGAGGAGTCCAGGAAATTTCCCTCGAGCGATGCCCATATGGGCA	6241
Db	5102	GAGGGGCTGTGAGTGGATGAACCGGCTGATAGCGTTCCGTTCCGCGGGTAAACACGTC	5161	Qy	6242	CGCCGGATTACAACCTCTTCTAGAGTCTTGGAAAGGACCCGGAATACGTCCTCTCCA	6301
Qy	5162	TCCCCACGCACTATGTGCTGAGAGGACGCTGACAGAGTGTCACTCAGATCTCTCT	5221	Db	6242	CGCCGGATTACAACCTCTTCTAGAGTCTTGGAAAGGACCCGGAATACGTCCTCTCCA	6301
Db	5162	TCCCCACGCACTATGTGCTGAGAGGACGCTGACAGAGTGTCACTCAGATCTCTCT	5221	Qy	6302	GTGTTACACGGGTGTCATTCGCGCTCCAAAGGCCCTTCGATACCACTCCAGGAGG	6361
Qy	5222	AGTCTTACCATCACTCAGCTCTGAGAGGCTTCCAGGTGGATCAACGAGGACTGCTCC	5281	Db	6302	GTGTTACACGGGTGTCATTCGCGCTCCAAAGGCCCTTCGATACCACTCCAGGAGG	6361
Db	5222	AGTCTTACCATCACTCAGCTCTGAGAGGCTTCCAGGTGGATCAACGAGGACTGCTCC	5281	Qy	6362	AAGAGGACGGTGTCTGTGAGATCTACCGTGTCTTCTGCGCTTGGCGAGCTCGCCACA	6421
Qy	5282	ACGCCATGCTCCGGCTCGTGGCTTAAGAGATGTTTGGGATTTGGATATGACGCGTGTGACT	5341	Db	6362	AAGAGGACGGTGTCTGTGAGATCTACCGTGTCTTCTGCGCTTGGCGAGCTCGCCACA	6421
Db	5282	ACGCCATGCTCCGGCTCGTGGCTTAAGAGATGTTTGGGATTTGGATATGACGCGTGTGACT	5341	Qy	6422	AAGACCTTTCGAGCTCGMAATTCGTGCGCGCTCGACAGCGGCAACCGGCTCTCTCT	6481
Qy	5342	GATTTCAAGACTGCTGCTCAAGTCCAGTCTGCGCGGATTTGGCGGAGTCCCTCTCTTC	5401	Db	6422	AAGACCTTTCGAGCTCGMAATTCGTGCGCGCTCGACAGCGGCAACCGGCTCTCTCT	6481
Db	5342	GATTTCAAGACTGCTGCTCAAGTCCAGTCTGCGCGGATTTGGCGGAGTCCCTCTCTTC	5401	Qy	6482	GAACAGCCCTCCGACGAGCGGGAATCCGAGTTCGACGTTGAGTCTGCTCTCAATGCCC	6541
Qy	5402	TCAATGCAAGTGGGTACAGGAGGCTTGGCGGGGACGGCATCATGCAAAACCACTGCG	5461	Db	6482	GAACAGCCCTCCGACGAGCGGGAATCCGAGTTCGACGTTGAGTCTGCTCTCAATGCCC	6541
Db	5402	TCAATGCAAGTGGGTACAGGAGGCTTGGCGGGGACGGCATCATGCAAAACCACTGCG	5461	Qy	6542	CCCCTTGAGGGGAGCGCGGGGATCCCGATCTCAGCGAGCGGTCTTGGTCTACCGTAGC	6601
Qy	5462	CCATGTGGAGCACAGATCACCGGACATGTGAAAAAATGTTTCCATGAGGATCGTGGGCT	5521	Db	6542	CCCCTTGAGGGGAGCGCGGGGATCCCGATCTCAGCGAGCGGTCTTGGTCTACCGTAGC	6601
Db	5462	CCATGTGGAGCACAGATCACCGGACATGTGAAAAAATGTTTCCATGAGGATCGTGGGCT	5521				

Qy	6602	GAGGAGCTAGTGAGGACGTCGTCTGCTCGATCGTCTACATGACAGCGCCCTG	6661
Db	6602	GAGGAGCTAGTGAGGACGTCGTCTGCTCGATCGTCTACATGACAGCGCCCTG	6661
Qy	6662	ATCAGCGCATCGCTCGGAGGAAACCAAGCTGCCATCAATGACACTCTTTTG	6721
Db	6662	ATCAGCGCATCGCTCGGAGGAAACCAAGCTGCCATCAATGACACTCTTTTG	6721
Qy	6722	CTCGCTACACAACTTGGTCTATGCTACACATCTCGAGCGCAAGCTCGGCGAAG	6781
Db	6722	CTCGCTACACAACTTGGTCTATGCTACACATCTCGAGCGCAAGCTCGGCGAAG	6781
Qy	6782	AAGTCACTTTGACAGCTGCGAGTCTTGACAGCACTACCGGAGCTGCTCAAGGAG	6841
Db	6782	AAGTCACTTTGACAGCTGCGAGTCTTGACAGCACTACCGGAGCTGCTCAAGGAG	6841
Qy	6842	ATGAAGCGAAGCGTCCACAGTTAAGGCTAACTTCTATCCGTTGAGGAAGCTGTAAG	6901
Db	6842	ATGAAGCGAAGCGTCCACAGTTAAGGCTAACTTCTATCCGTTGAGGAAGCTGTAAG	6901
Qy	6902	CTGACGCCCCACATTCGGCCAGATCTAAATTTGGCTATGGGCAAGAGCTCCGGAAC	6961
Db	6902	CTGACGCCCCACATTCGGCCAGATCTAAATTTGGCTATGGGCAAGAGCTCCGGAAC	6961
Qy	6962	CTATCCAGCAAGCGCTTAACCACTCGCTCGTGTGGAAGGACTTGTGGAAGACACT	7021
Db	6962	CTATCCAGCAAGCGCTTAACCACTCGCTCGTGTGGAAGGACTTGTGGAAGACACT	7021
Qy	7022	GAGACACCAATTGACACCAATCATGCGCAAAATGAGGTTTCTCGCTCCAAACAGAG	7081
Db	7022	GAGACACCAATTGACACCAATCATGCGCAAAATGAGGTTTCTCGCTCCAAACAGAG	7081
Qy	7082	AAGGGGGCGCAAGCAGCTCGCTTATCGTATTCACAGTTTGGGGTTCGTGTGTC	7141
Db	7082	AAGGGGGCGCAAGCAGCTCGCTTATCGTATTCACAGTTTGGGGTTCGTGTGTC	7141
Qy	7142	GAGAAATGGCCCTTTAGATGTGCTTCCACCTCGCTCAGGCGTGATGGGCTCTTCA	7201
Db	7142	GAGAAATGGCCCTTTAGATGTGCTTCCACCTCGCTCAGGCGTGATGGGCTCTTCA	7201
Qy	7202	TACGGATTCCAAATCTCTCTGGAAGCGGCTCGATTCCTGTTGAAATGCTTGAAGCG	7261
Db	7202	TACGGATTCCAAATCTCTCTGGAAGCGGCTCGATTCCTGTTGAAATGCTTGAAGCG	7261
Qy	7262	AAGAAATGCGCTATGGGCTTGCATATGACACCGCTGTTTGAATCAACGCTCAG	7321
Db	7262	AAGAAATGCGCTATGGGCTTGCATATGACACCGCTGTTTGAATCAACGCTCAG	7321
Qy	7322	AATGACATCGGTTGAGGAGTCAATCTACCAATGTTGACTTGGCCCGGAGCCAGA	7381
Db	7322	AATGACATCGGTTGAGGAGTCAATCTACCAATGTTGACTTGGCCCGGAGCCAGA	7381
Qy	7382	CAGGCCATAGGTCGCTCACAGAGCGGCTTACATCGGGGCGCCCTGACTTAATCTAAA	7441
Db	7382	CAGGCCATAGGTCGCTCACAGAGCGGCTTACATCGGGGCGCCCTGACTTAATCTAAA	7441
Qy	7442	GGGAGAACTCGGGCTATCGCGGTGCGCGAGCGGTGACTGACAGCAGCTCGGT	7501
Db	7442	GGGAGAACTCGGGCTATCGCGGTGCGCGAGCGGTGACTGACAGCAGCTCGGT	7501
Qy	7502	AATACCTTCACATGTTACTGAAGCGCTCGGCTGTCGAGCTGCGAAGCTCCAGGAC	7561
Db	7502	AATACCTTCACATGTTACTGAAGCGCTCGGCTGTCGAGCTGCGAAGCTCCAGGAC	7561
Qy	7562	TGACAGATGCTGATGCGGAGAGCACTTCTGCTTATCTGTGAAAGCGGGGACCCAA	7621
Db	7562	TGACAGATGCTGATGCGGAGAGCACTTCTGCTTATCTGTGAAAGCGGGGACCCAA	7621
Qy	7622	GAGGACGAGGAGCTTACGGGCTTACGAGGCTATGACTAGATCTGCCCCCCT	7681
Db	7622	GAGGACGAGGAGCTTACGGGCTTACGAGGCTATGACTAGATCTGCCCCCCT	7681
Qy	7682	GGGACCGCCCAACCAAGATACGACTTGAGTTGATAACATCATGCTCCTCCAATGTG	7741

Db	7682	GGGACCGCCCAACCAAGATACGACTTGGAGTTGATAAATCATGCTCCTCAATGTG	7741
Qy	7742	TCAGTCGGCGCAGATGCTGCGCAAAAGGTTACTATCTCACCGTGCACCCACACC	7801
Db	7742	TCAGTCGGCGCAGATGCTGCGCAAAAGGTTACTATCTCACCGTGCACCCACACC	7801
Qy	7802	CCCTTTGCGCGGCTGCGTGGGAGAGCAGCTAGACACACTCCAGTCAATCTCGCTAGGC	7861
Db	7802	CCCTTTGCGCGGCTGCGTGGGAGAGCAGCTAGACACACTCCAGTCAATCTCGCTAGGC	7861
Qy	7862	AACATCATGATATGCGGCCACCTTGTGGGCAAGGATGATCTCTGATGACTCATTTCTTC	7921
Db	7862	AACATCATGATATGCGGCCACCTTGTGGGCAAGGATGATCTCTGATGACTCATTTCTTC	7921
Qy	7922	TCATCTCTTACGCTCAGGAACAACCTTGAAAGCCCTAGATTGTTCAGATCTACGGGCGC	7981
Db	7922	TCATCTCTTACGCTCAGGAACAACCTTGAAAGCCCTAGATTGTTCAGATCTACGGGCGC	7981
Qy	7982	TGTTACTTCCATTTGAGCCACTTGCACCTACCTCAGATCATTTCAACGACTCCAGCCCTTAGC	8041
Db	7982	TGTTACTTCCATTTGAGCCACTTGCACCTACCTCAGATCATTTCAACGACTCCAGCCCTTAGC	8041
Qy	8042	GCAATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGTTGCTTCATGCTCAGG	8101
Db	8042	GCAATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGTTGCTTCATGCTCAGG	8101
Qy	8102	AACTTTGGGTTACCGCCCTTGCAGTCTCGAGACATCGGGCCAGAGTGTCCGCGCTAGG	8161
Db	8102	AACTTTGGGTTACCGCCCTTGCAGTCTCGAGACATCGGGCCAGAGTGTCCGCGCTAGG	8161
Qy	8162	CTACTCTCCAGGGGGGAGGCTGCTGCTTGTGCAAGTACCTCTTCAACTGGGCACTA	8221
Db	8162	CTACTCTCCAGGGGGGAGGCTGCTGCTTGTGCAAGTACCTCTTCAACTGGGCACTA	8221
Qy	8222	AGGACCAAGCTCAAACTCACTCCAAATCCCGGCTGCGTCCAGTTGATTTATCCAGCTGG	8281
Db	8222	AGGACCAAGCTCAAACTCACTCCAAATCCCGGCTGCGTCCAGTTGATTTATCCAGCTGG	8281
Qy	8282	TTCTGTTGCTGTTTACAGCGGGGAGACATATATCAGGCTGTCTGTCGCCAGCCCGC	8341
Db	8282	TTCTGTTGCTGTTTACAGCGGGGAGACATATATCAGGCTGTCTGTCGCCAGCCCGC	8341
Qy	8342	TGCTTCACTGCTGCTTACTCTTCTTCTGTTAGGGGTAGGCTATCTACTCTCCCAAC	8401
Db	8342	TGCTTCACTGCTGCTTACTCTTCTTCTGTTAGGGGTAGGCTATCTACTCTCCCAAC	8401
Qy	8402	CGATGAAACGGGAGCTTAAACACTCCAGGCAATAGGCAATCTCTGTTTCTCTTTT	8461
Db	8402	CGATGAAACGGGAGCTTAAACACTCCAGGCAATAGGCAATCTCTGTTTCTCTTTT	8461
Qy	8462	CCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	8521
Db	8462	TTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	8521
Qy	8522	TCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	8581
Db	8517	TTCCCAATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	8576
Qy	8582	GCTGTGAAAGGTCCTGAGCGCTTGAATGTCAGAGAGTGTGATGCTGCTCTCTGAG	8641
Db	8577	GCTGTGAAAGGTCCTGAGCGCTTGAATGTCAGAGAGTGTGATGCTGCTCTCTGAG	8636
Qy	8642	ATCAAGT 8648	
Db	8637	ATCAAGT 8643	

RESULT 4  
US-10-789-355-7  
; Sequence 7, Application US/10789355  
; GENERAL INFORMATION:  
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.

; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM

; FILE REFERENCE: 13/083

; CURRENT APPLICATION NUMBER: US/10/789,355

; PRIOR FILING DATE: 2004-02-27

; PRIOR APPLICATION NUMBER: US/10/029,907

; PRIOR FILING DATE: 2001-12-21

; PRIOR APPLICATION NUMBER: 60/257,857

; PRIOR FILING DATE: 2000-12-22

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 7

; LENGTH: 8638

; TYPE: DNA

; ORGANISM: HCV

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1802)...(8407)

; US-10-789-355-7

Query Match 99.2%; Score 8578.2; DB 1; Length 8638;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 8610; Conservative 0; Mismatches 28; Indels 10; Gaps 1;

QY	1	GCACGCCGCCGATTGGGGGCGACACTCCACATAGATCACTCCCTGTGAGGAACACTACTG	60
DB	1	GCACGCCGCCGATTGGGGGCGACACTCCACATAGATCACTCCCTGTGAGGAACACTACTG	60
QY	61	TCCTCAGCGAAGAAAGCGTTAGCCATGGCGTGTAGTATGATGTGCTGAGCCTCCAGGAC	120
DB	61	TCCTCAGCGAAGAAAGCGTTAGCCATGGCGTGTAGTATGATGTGCTGAGCCTCCAGGAC	120
QY	121	CCCCCTCCCGGAGAGCCATAGTGTCTCGGAAACCGGTGACTACACCGGAATTCGCCAG	180
DB	121	CCCCCTCCCGGAGAGCCATAGTGTCTCGGAAACCGGTGACTACACCGGAATTCGCCAG	180
QY	181	GACGACCGGTCTCTTCTTGATCAACCCGCTCAATCCCTGGAGATTTGGCGGTGCCCCC	240
DB	181	GACGACCGGTCTCTTCTTGATCAACCCGCTCAATCCCTGGAGATTTGGCGGTGCCCCC	240
QY	241	GCAGACTGTAGCCGAGTAGTGTGGGTGCGAAAGCGCTTGTGGTATCTGCTGTATAGG	300
DB	241	GCAGACTGTAGCCGAGTAGTGTGGGTGCGAAAGCGCTTGTGGTATCTGCTGTATAGG	300
QY	301	GTCTTGGAGTCCCGGAGGTCTGTAGACCGGTGACCAATCCCTAAAC	360
DB	301	GTCTTGGAGTCCCGGAGGTCTGTAGACCGGTGACCAATCCCTAAAC	360
QY	361	CTCAAGAAAAAACAAGGCGCGCCATGATTGAACAAGATGGAATGCGACGAGTTCTC	420
DB	361	CTCAAGAAAAAACAAGGCGCGCCATGATTGAACAAGATGGAATGCGACGAGTTCTC	420
QY	421	CGGCGCTTGGGTGGAGAGCTATTGGGTATGACTGGGCAACAAGCAATCGGCTGCT	480
DB	421	CGGCGCTTGGGTGGAGAGCTATTGGGTATGACTGGGCAACAAGCAATCGGCTGCT	480
QY	481	CTGATCCGCGGTTCCTCCGCTGTACGCGAGGGGCGCCGGTCTTTTGTCAAGACCG	540
DB	481	CTGATCCGCGGTTCCTCCGCTGTACGCGAGGGGCGCCGGTCTTTTGTCAAGACCG	540
QY	541	ACCTGTCCGCTGCCCTGAATGAACCTGACGACGAGGCGCGGCTATCGTGGCTGGCCA	600
DB	541	ACCTGTCCGCTGCCCTGAATGAACCTGACGACGAGGCGCGGCTATCGTGGCTGGCCA	600
QY	601	CGACGGCGTTCCTTGGCGAGCTGTGCTGCAAGTGTGACTGAAGCGGGGAAGGACTGGC	660
DB	601	CGACGGCGTTCCTTGGCGAGCTGTGCTGCAAGTGTGACTGAAGCGGGGAAGGACTGGC	660
QY	661	TGCTATTGGGGAAGTCCCGGGGAGGATCTCCTGTCTCATCTCACTTGTCTCTCGCGAGA	720
DB	661	TGCTATTGGGGAAGTCCCGGGGAGGATCTCCTGTCTCATCTCACTTGTCTCTCGCGAGA	720
QY	721	AAGTATCCATCATGGCTGATGCAATGCGGGGCTGTCATACGCTTGATCCGGCTACCTGCC	780

DB	721	AAGTATCCATCATGGCTGATGCAATGCGGGCTGTCATACGCTTGCATCGGCTACCTGCC	780
QY	781	CATTGACCAACCAAGCAAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCGGTC	840
DB	781	CATTGACCAACCAAGCAAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCGGTC	840
QY	841	TTGTGATCAGGATGATCTGGACGAAGAGCATCAGGGCTCGCGCAGCCGAACCTGTTCCG	900
DB	841	TTGTGATCAGGATGATCTGGACGAAGAGCATCAGGGCTCGCGCAGCCGAACCTGTTCCG	900
QY	901	CCAGGCTCAAGGCGCGCATCGCCGACGAGGAGTCTCGTGTGACCCATGCGGATGCT	960
DB	901	CCAGGCTCAAGGCGCGCATCGCCGACGAGGAGTCTCGTGTGACCCATGCGGATGCT	960
QY	961	GCTTCCCGAATATCATGTGGAATAATGCGGCTTCTTGGATTCTCGACTGTGGCCGGC	1020
DB	961	GCTTCCCGAATATCATGTGGAATAATGCGGCTTCTTGGATTCTCGACTGTGGCCGGC	1020
QY	1021	TGGGTGTGGCGACCGCTTATCAGGACATAGCGTGTGGCTACCGGTGATATTGCTGAAGAGC	1080
DB	1021	TGGGTGTGGCGACCGCTTATCAGGACATAGCGTGTGGCTACCGGTGATATTGCTGAAGAGC	1080
QY	1081	TTGGCGGGAATGGGCTCACCGCTTCTCGTGTGCTTACGGTATCGCGCTCCGATTCGC	1140
DB	1081	TTGGCGGGAATGGGCTCACCGCTTCTCGTGTGCTTACGGTATCGCGCTCCGATTCGC	1140
QY	1141	AGCGCATCGCTTCTATCGCTTCTTACGAGTCTTCTGAGTTCGCGCCACAGATGTTAA	1200
DB	1141	AGCGCATCGCTTCTATCGCTTCTTACGAGTCTTCTGAGTTCGCGCCACAGATGTTAA	1200
QY	1201	CAGACCAACAAAGGTTTCCCTCTAGCGGATCAATTCGCCGCCGCCCTTAAAGTTACTGG	1260
DB	1201	CAGACCAACAAAGGTTTCCCTCTAGCGGATCAATTCGCCGCCGCCCTTAAAGTTACTGG	1260
QY	1261	CGAAGCGCTTGAATTAAGCGCGGTGCGTTGCTATATGTTATTTTCCACCATATT	1320
DB	1261	CGAAGCGCTTGAATTAAGCGCGGTGCGTTGCTATATGTTATTTTCCACCATATT	1320
QY	1321	GCGGTCTTTTGGCAATGTAGGCGCCGGAACCTCGCCCTGCTCTTCTGACGAGCATTC	1380
DB	1321	GCGGTCTTTTGGCAATGTAGGCGCCGGAACCTCGCCCTGCTCTTCTGACGAGCATTC	1380
QY	1381	TAGGGGTCTTTCCCTCTCGCAAGAAATCAAGGTCTGTTGAATGTCGTGAAGAAAC	1440
DB	1381	TAGGGGTCTTTCCCTCTCGCAAGAAATCAAGGTCTGTTGAATGTCGTGAAGAAAC	1440
QY	1441	AGTTCTCTGGAAGCTTCTTGAAGCAACACACGTCTGTAGCGACCTTTGAGGCGAGG	1500
DB	1441	AGTTCTCTGGAAGCTTCTTGAAGCAACACACGTCTGTAGCGACCTTTGAGGCGAGG	1500
QY	1501	GAACCCCGCCTGCGACAGGTGCTCTGCGGCCAAGAACACCGTGTATAAGATACACC	1560
DB	1501	GAACCCCGCCTGCGACAGGTGCTCTGCGGCCAAGAACACCGTGTATAAGATACACC	1560
QY	1561	TGCAAGGCGGCAACACCCAGTGCACGTTGTGAGTTGGATGTTGTGGAAGAGTCAA	1620
DB	1561	TGCAAGGCGGCAACACCCAGTGCACGTTGTGAGTTGGATGTTGTGGAAGAGTCAA	1620
QY	1621	ATGGCTCTCTCAAGGCTATTCAAACAGGGCTGAGGATGCCAGAGGTACCCCATTCG	1680
DB	1621	ATGGCTCTCTCAAGGCTATTCAAACAGGGCTGAGGATGCCAGAGGTACCCCATTCG	1680
QY	1681	TATGGGATCTGATCTGGGCTCTCGGTGACATGCTTTACATGTTTGTAGTTCAGGTTAAA	1740
DB	1681	TATGGGATCTGATCTGGGCTCTCGGTGACATGCTTTACATGTTTGTAGTTCAGGTTAAA	1740
QY	1741	AAACGCTTAGGGCCCCCGAACCAACCGGGACGTGGTCTTCTTTGAAAAACAAGATAATAC	1800
DB	1741	AAACGCTTAGGGCCCCCGAACCAACCGGGACGTGGTCTTCTTTGAAAAACAAGATAATAC	1800
QY	1801	CATGACCGGGAGATGGGAGCATCGTGGCGAGGCGGGTTCCTGTAAGGTCTGATCTCTT	1860

1801 CATGGACGGGAGATGGCAGCATCTGTGGGAGCGCGGTTTTTCGTAGGTCTGATACCTCTT 1860  
1861 GACCTTTGTACCCGACTATTAAGCTGTTCCTCGTAGGCTCATATGTTGTTTACAAATATTT 1920  
1861 GACCTTTGTACCCGACTATTAAGCTGTTCCTCGTAGGCTCATATGTTGTTTACAAATATTT 1920  
1921 TATCACAGGGCCGAGGACACATTGCAAGTGTGGATCCCCCCCCCTCAACGTTTCGGGGGGG 1980  
1921 TATCACAGGGCCGAGGACACATTGCAAGTGTGGATCCCCCCCCCTCAACGTTTCGGGGGGG 1980  
1981 CCGCGATGCGGTTCATCTCTCTCAAGTGTGGATCCACCCAGAGCTAACTTTTACCATCAC 2040  
1981 CCGCGATGCGGTTCATCTCTCTCAAGTGTGGATCCACCCAGAGCTAACTTTTACCATCAC 2040  
2041 CAAAATCTTGCTCGCCATCTCGGTCCACTCATGTTGGTCCAGGCTGGTATTAACCAAGT 2100  
2041 CAAAATCTTGCTCGCCATCTCGGTCCACTCATGTTGGTCCAGGCTGGTATTAACCAAGT 2100  
2101 GCCGTACTTCTGCGGCGACACAGGGCTCATTCGTGATGATGCTCGTGGGAAAGTTGC 2160  
2101 GCCGTACTTCTGCGGCGACACAGGGCTCATTCGTGATGATGCTCGTGGGAAAGTTGC 2160  
2161 TGGGGGTCAATTAATGCTCAAAATGGCTCTCATGAAGTTGGCCGCACTGACAGGTACGTACGT 2220  
2161 TGGGGGTCAATTAATGCTCAAAATGGCTCTCATGAAGTTGGCCGCACTGACAGGTACGTACGT 2220  
2221 TTAATGACATCTCACCCACTGCGGGACTGGGCCACCGGGGCTACGAGACCTTCGGGT 2280  
2221 TTAATGACATCTCACCCACTGCGGGACTGGGCCACCGGGGCTACGAGACCTTCGGGT 2280  
2281 GGCAGTTGAGCCCGTCTCTCTGATATGGAGCAAGGTTTATACCTTGGGGGGCAGA 2340  
2281 GGCAGTTGAGCCCGTCTCTCTGATATGGAGCAAGGTTTATACCTTGGGGGGCAGA 2340  
2341 CACCGCGCGGTGTGGGACATCATCTTGGGCTTGGGCTTCCCGCGCAGAGGGGAGGGA 2400  
2341 CACCGCGCGGTGTGGGACATCATCTTGGGCTTGGGCTTCCCGCGCAGAGGGGAGGGA 2400  
2401 GATACATCTGGGACCGGCGACAGCCCTTGAAGGCGAGGGGTGGGACTCTCTCGGCTTAT 2460  
2401 GATACATCTGGGACCGGCGACAGCCCTTGAAGGCGAGGGGTGGGACTCTCTCGGCTTAT 2460  
2461 TAGCGGCTACTCCCAACAGACCGGAGGCTTACTTGGCTGCATCATCATAGCCCTCACAGG 2520  
2461 TAGCGGCTACTCCCAACAGACCGGAGGCTTACTTGGCTGCATCATCATAGCCCTCACAGG 2520  
2521 CCGGGACAGGAACACAGGTCGAGGGGAGGTCGAAGTGGTCTCCACCGCAACAAATCTTT 2580  
2521 CCGGGACAGGAACACAGGTCGAGGGGAGGTCGAAGTGGTCTCCACCGCAACAAATCTTT 2580  
2581 CTTGGCGACTGGCTCAATGGCGTGTGTTGGAATGTGGAATGTGGAATGTGGAATGTGGAAT 2640  
2581 CTTGGCGACTGGCTCAATGGCGTGTGTTGGAATGTGGAATGTGGAATGTGGAATGTGGAAT 2640  
2641 CTTGGCGACTGGCTCAATGGCGTGTGTTGGAATGTGGAATGTGGAATGTGGAATGTGGAAT 2700  
2641 CTTGGCGACTGGCTCAATGGCGTGTGTTGGAATGTGGAATGTGGAATGTGGAATGTGGAAT 2700  
2701 CCGTGGCAAGCGCCCCCGGGGCGCGTCTTGGACACCATGCACTTGGCGGCGACTCGGA 2760  
2701 CCGTGGCAAGCGCCCCCGGGGCGCGTCTTGGACACCATGCACTTGGCGGCGACTCGGA 2760  
2761 CTTTATCTTGGTACAGAGGATGCGGATGTCTATTCGGGTGGCGGGGGCGGACAGCAG 2820  
2761 CTTTATCTTGGTACAGAGGATGCGGATGTCTATTCGGGTGGCGGGGGCGGACAGCAG 2820  
2821 GGGAGGCTACTCTCCCCCGGGCCGCTCTCTACTTGAAGGGCTCTCTCGGGCGGTCCACT 2880  
2821 GGGAGGCTACTCTCCCCCGGGCCGCTCTCTACTTGAAGGGCTCTCTCGGGCGGTCCACT 2880  
2881 GCTCGCCCTCGGGGACCGCTGTGGGCTCTTTTCGGGCTGCGGTGTGACACCGGGGGGT 2940  
2881 GCTCGCCCTCGGGGACCGCTGTGGGCTCTTTTCGGGCTGCGGTGTGACACCGGGGGGT 2940

2941 TCCGAAGCGGTGGACTTTGTACCCGTGAGTCTATGGAAACCACTATGCGGTCCCGGT 3000  
2941 TCCGAAGCGGTGGACTTTGTACCCGTGAGTCTATGGAAACCACTATGCGGTCCCGGT 3000  
3001 CTTTCA CGGACAACTCGTCCCTCCGCGGTACCGCAGACATTCAGAGTGGCCCATCTACA 3060  
3001 CTTTCA CGGACAACTCGTCCCTCCGCGGTACCGCAGACATTCAGAGTGGCCCATCTACA 3060  
3061 CGCCCTACTGTTAGGGGCAAGACACTAAGGTGCGGCTGCTATGACGCCCAAGGTA 3120  
3061 CGCCCTACTGTTAGGGGCAAGACACTAAGGTGCGGCTGCTATGACGCCCAAGGTA 3120  
3121 TAAAGTGTCTGCTGAACCCGTCGCTCCGCCACCCCTAGGTTCCTGGGGCGGTATATGTC 3180  
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3181 TAAAGCA CATGTTATCGACCCCTAA CATAGAACCGGGGTAAAGCA CATCA CACGGGTGC 3240  
3181 TAAAGCA CATGTTATCGACCCCTAA CATAGAACCGGGGTAAAGCA CATCA CACGGGTGC 3240  
3241 CCCATCAGCTACTCCACTATGTCAGTGCACCTCAACTGACTCGACCACTATCTTGGGCAT 3300  
3241 CCCATCAGCTACTCCACTATGTCAGTGCACCTCAACTGACTCGACCACTATCTTGGGCAT 3300  
3301 CTATGACATCATTAATATGTCAGTGCACCTCAACTGACTCGACCACTATCTTGGGCAT 3360  
3301 CTATGACATCATTAATATGTCAGTGCACCTCAACTGACTCGACCACTATCTTGGGCAT 3360  
3361 CGGCA CAGTCTCTGGA CCAAGCGGAG CCGCTGGAGCGGACTCGTCTGCTCGCCACCGC 3420  
3361 CGGCA CAGTCTCTGGA CCAAGCGGAG CCGCTGGAGCGGACTCGTCTGCTCGCCACCGC 3420  
3421 TAGGCTCGGGATCGGTACCGTCCACATCAACCAATCGAGAGGTGCTCTGTCCAG 3480  
3421 TAGGCTCGGGATCGGTACCGTCCACATCAACCAATCGAGAGGTGCTCTGTCCAG 3480  
3481 CACTGAGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACCATCAAGGGGGGGAG 3540  
3481 CACTGAGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACCATCAAGGGGGGGAG 3540  
3541 GCACCTCATTTTCTGCAATTCGAAGAAATGTGATGAGTCCGCGGAAAGTGTCCGG 3600  
3541 GCACCTCATTTTCTGCAATTCGAAGAAATGTGATGAGTCCGCGGAAAGTGTCCGG 3600  
3601 CTTGGAATCAATGCTGTAGCATATTA CCGGGGCTTGTATGATCGGTCAATCAACTAG 3660  
3601 CTTGGAATCAATGCTGTAGCATATTA CCGGGGCTTGTATGATCGGTCAATCAACTAG 3660  
3661 CCGGAGAGTCAATGCTGTAACCAAGCA CGCTCTAATGA CCGGCTTTTACCGGCGATTTTGA 3720  
3661 CCGGAGAGTCAATGCTGTAACCAAGCA CGCTCTAATGA CCGGCTTTTACCGGCGATTTTGA 3720  
3721 CTTAGTGTATGATGCAATGATGTCAC CAGACAGTGCAGCTTTCAGCTTCGACCCGAC 3780  
3721 CTTAGTGTATGATGCAATGATGTCAC CAGACAGTGCAGCTTTCAGCTTCGACCCGAC 3780  
3781 CTTTACCAATTGAGA CAGACCGGTCCCA CAAGACCGGTGTACGCTCGCAGCGGGAGG 3840  
3781 CTTTACCAATTGAGA CAGACCGGTCCCA CAAGACCGGTGTACGCTCGCAGCGGGAGG 3840  
3841 CAGGACTGTTAGGGGAGGATGGGCAATTTACAGTTTGTGACTCCAGGAGAACGGCCCTC 3900  
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3901 GGGCATGTTTCTGATCTCTCGGCTGTGTCAGTGTGATGACCGGGGCTGTGCTTGGTACGA 3960  
3901 GGGCATGTTTCTGATCTCTCGGCTGTGTCAGTGTGATGACCGGGGCTGTGCTTGGTACGA 3960  
3961 GCTCAGCCCGCGGAGACCTCAGTTAGGTTGGGGCTTACCTTAAACACACACAGGGTTGCC 4020  
3961 GCTCAGCCCGCGGAGACCTCAGTTAGGTTGGGGCTTACCTTAAACACACACAGGGTTGCC 4020



QY	4021	CGTCTGCCAGGACCACTCTGGAGTTCTGGGAGAGCGTCTTTTACAGGCTCAACCCACATAGA	4080	Db	5101	GGAGGGGCTGTGCAGTGGATGAACCGGCTGATAGCGTTGCTTCGCGGGTAACCAAGT	5160
Db	4021	CGTCTGCCAGGACCACTCTGGAGTTCTGGGAGGCGTCTTTTACAGGCTCAACCCACATAGA	4080	QY	5161	CTCCCCCAGCAGCTATGTGCTGAGAGGAGCGCTGCACAGCTGTCACTCAGATCCTCTC	5220
QY	4081	CGCCCATTTCTTGTCCAGACTAAGCAGGAGAGACAATTTCCCTTACCTGTGTAGCATATA	4140	Db	5161	CTCCCCCAGCAGCTATGTGCTGAGAGGAGCGCTGCACAGCTGTCACTCAGATCCTCTC	5220
Db	4081	CGCCCATTTCTTGTCCAGACTAAGCAGGAGGAGAGACAATTTCCCTTACCTGTGTAGCATATA	4140	QY	5221	TAGTCTTACCATCACTCAGCTGCTGAAGAGGCTTCCACAGTGGATCAACAGGAGCTGCTC	5280
QY	4141	CCAGGCTACGGTGTGGCCAGGCTCAGGCTCCAGCTCCAGCTCCATCGTGGGACCAATGTGGAA	4200	Db	5221	TAGTCTTACCATCACTCAGCTGCTGAAGAGGCTTCCACAGTGGATCAACAGGAGCTGCTC	5280
Db	4141	CCAGGCTACGGTGTGGCCAGGCTCAGGCTCCAGCTCCAGCTCCATCGTGGGACCAATGTGGAA	4200	QY	5281	CACGCCATGCTCCGGCTCGTGGCTAAGAGATGTTTGGATGGGTATGCACGGTGTGAC	5340
QY	4201	GTGTCTCATACGGCTAAGCTTACGTGCAAGGCGCAAGCCCTCTGTATAGGCTGGG	4260	Db	5281	CACGCCATGCTCCGGCTCGTGGCTAAGAGATGTTTGGATGGGTATGCACGGTGTGAC	5340
Db	4201	GTGTCTCATACGGCTAAGCTTACGTGCAAGGCGCAAGCCCTCTGTATAGGCTGGG	4260	QY	5341	TGATTTCAAGACCTCGGCTCCAGTCCAGCTCTGCGCGGATTTGCCGGAGTCCCTCTT	5400
QY	4261	AGCCGTTCAAAAAGAGGTTACTACACACACCCCATAAACCAATATCATATGCGATGCAT	4320	Db	5341	TGATTTCAAGGCTCGGCTCCAGTCCAGCTCTGCGCGGATTTGCCGGAGTCCCTCTT	5400
Db	4261	AGCCGTTCAAAAAGAGGTTACTACACACACCCCATAAACCAATATCATATGCGATGCAT	4320	QY	5401	CTCATGTCAACGCTGGGTACAAGGGAGTCTGGCGGGCGACCGCATCATGCAAAACACCTG	5460
QY	4321	GTCCGCTGACCTGGAGTCTGACGAGCACTCGGTGCTGGTAGGCGGAGTCTTAGCAGC	4380	Db	5401	CTCATGTCAACGCTGGGTACAAGGGAGTCTGGCGGGCGACCGCATCATGCAAAACACCTG	5460
Db	4321	GTCCGCTGACCTGGAGTCTGACGAGCACTCGGTGCTGGTAGGCGGAGTCTTAGCAGC	4380	QY	5461	CCCATGTGGAGCACAGATCAACCGGACATGTGAAAAAATGTTCCATGAGGATCGTGGGGC	5520
QY	4381	TCTGGCGCGTATTTGGCTGACAAACAGCAGCGTGGTCAATTTGGGCGAGGATCATCTTGTG	4440	Db	5461	CCCATGTGGAGCACAGATCAACCGGACATGTGAAAAAATGTTCCATGAGGATCGTGGGGC	5520
Db	4381	TCTGGCTGCTATTTGGCTGACAAACAGCAGCGTGGTCAATTTGGGCGAGGATCATCTTGTG	4440	QY	5521	TAGGACCTGTAGTAACAGCTGSCATGGAATTCCTCCCATTAACCGGTACACCAACCGGCCC	5580
QY	4441	CGGAAAGCGCGCATCATTTCCGACAGGGAAGTCTTTTACCGGGAGTTCATGAGATGGA	4500	Db	5521	TAGGACCTGTAGTAACAGCTGSCATGGAATTCCTCCCATTAACCGGTACACCAACCGGCCC	5580
Db	4441	CGGAAAGCGCGCATCATTTCCGACAGGGAAGTCTTTTACCGGGAGTTCATGAGATGGA	4500	QY	5581	CTGACAGCGCTCCCGCGGCCAAATTTATTTAGGGCGCTGTGGCGGGTGGCTGTGAGGA	5640
QY	4501	AGAGTGGCTCACAATCTCCCTTACATCGAAGGGAATCGAGCTCGCGCAACAAATTCAT	4560	Db	5581	CTGACAGCGCTCCCGCGGCCAAATTTATTTAGGGCGCTGTGGCGGGTGGCTGTGAGGA	5640
Db	4501	AGAGTGGCTCACAATCTCCCTTACATCGAAGGGAATCGAGCTCGCGCAACAAATTCAT	4560	QY	5641	GTACCTGAGGTTACCGGGTGGGGATTTCCATCTACGAGCGGATGACCACTGACAA	5700
QY	4561	ACAGAGGCAATCGGTTGCTGCAACAGCAGCAACAGAGGAGGCTGCTGCTCCCGT	4620	Db	5641	GTACCTGAGGTTACCGGGTGGGGATTTCCATCTACGAGCGGATGACCACTGACAA	5700
Db	4561	ACAGAGGCAATCGGTTGCTGCAACAGCAGCAACAGAGGAGGCTGCTGCTCCCGT	4620	QY	5701	CGTAAAGTGGCGTCTGAGTTCCGGCCCGGAAATTTCTTACAGAAAGTGGATGGGGTGG	5760
QY	4621	GGTGGAAATCAAGTGGCGGACCTCGAAGCTTCTGGGCGAAGCATATGTGGAATTTCA	4680	Db	5701	CGTAAAGTGGCGTCTGAGTTCCGGCCCGGAAATTTCTTACAGAAAGTGGATGGGGTGG	5760
Db	4621	GGTGGAAATCAAGTGGCGGACCTCGAAGCTTCTGGGCGAAGCATATGTGGAATTTCA	4680	QY	5761	GTTCACAGGTAACGCTCCAGCGTCAAAACCCCTCTTACAGGAGGAGTCAATTCCTGT	5820
QY	4681	CAGGGGATCAATATTTAGCAGCTTGTCCACTCTGCTGCGCAACCCCGCGATAGCATC	4740	Db	5761	GTTCACAGGTAACGCTCCAGCGTCAAAACCCCTCTTACAGGAGGAGTCAATTCCTGT	5820
Db	4681	CAGGGGATCAATATTTAGCAGCTTGTCCACTCTGCTGCGCAACCCCGCGATAGCATC	4740	QY	5821	CGGGCTCAATCAATACCTCGGTTGGGTCAAGCTCCCATGCGAGCCCGAACCGGACGTAGC	5880
QY	4741	ACTGATGGCATTCACAGCTCTATCACAGCCGCTCACACCCGCTCACACCAACATACCTCTGTT	4800	Db	5821	CGGGCTCAATCAATACCTCGGTTGGGTCAAGCTCCCATGCGAGCCCGAACCGGACGTAGC	5880
Db	4741	ACTGATGGCATTCACAGCTCTATCACAGCCGCTCACACCCGCTCACACCAACATACCTCTGTT	4800	QY	5881	AGTGTCTCACTTCCATGCTCACCGACCTCCACATTTACGGCGGAGACGGCTAAAGCTAG	5940
QY	4801	TAAATCTCTGGGGGATGGGTGCGCGCCAACTTGTCTCTCCAGGCTGCTTCTGCTTT	4860	Db	5881	AGTGTCTCACTTCCATGCTCACCGACCTCCACATTTACGGCGGAGACGGCTAAAGCTAG	5940
Db	4801	TAAATCTCTGGGGGATGGGTGCGCGCCAACTTGTCTCTCCAGGCTGCTTCTGCTTT	4860	QY	5941	GCTGCGCAGGGGATCTCCCCCTCTTGGCCAGCTCATCAGCTAGCTGTCTGCGCC	6000
QY	4861	CGTAGGCGCGCATCGCTGGAGGCTGTGGCAGCATAGGCTTGGGAGGTGCTGT	4920	Db	5941	GCTGCGCAGGGGATCTCCCCCTCTTGGCCAGCTCATCAGCTAGCTGTCTGCGCC	6000
Db	4861	CGTAGGCGCGCATCGCTGGAGGCTGTGGCAGCATAGGCTTGGGAGGTGCTGT	4920	QY	6001	CTCTTTGAAGGCAATGCACTACCCGTCATGACTCCCGCGGACGCTCATCGAGGC	6060
QY	4921	GGATATTTTGGCAGGTTATGGAGCAGGGGTGGAGCGCGCTCGTGGCCCTTTAAGGTCA	4980	Db	6001	CTCTTTGAAGGCAATGCACTACCCGTCATGACTCCCGCGGACGCTCATCGAGGC	6060
Db	4921	GGATATTTTGGCAGGTTATGGAGCAGGGGTGGAGCGCGCTCGTGGCCCTTTAAGGTCA	4980	QY	6061	CAAACCTCTGTCGGCGCAGGAGATGGCGGGAACATCACCCCGTGGAGTCAGAGATTA	6120
QY	4981	GAGCGCGAGATGCCCTTCCACCGAGGACCTGGTTAACTACTCCCTGCTATCTCTCCCC	5040	Db	6061	CAAACCTCTGTCGGCGCAGGAGATGGCGGGAACATCACCCCGTGGAGTCAGAGATTA	6120
Db	4981	GAGCGCGAGATGCCCTTCCACCGAGGACCTGGTTAACTACTCCCTGCTATCTCTCCCC	5040	QY	6121	GCTAGTAATTTTGGACTCTTTTCGAGCGCTCTCAAGCGGAGGAGGATGAGAGGAAATATC	6180
QY	5041	TGGCGCCCTAGTCTGGGGTCTGTGCGCAGCGATCTCGCTCGGACGCTGGGGCCAGG	5100	Db	6121	GCTAGTAATTTTGGACTCTTTTCGAGCGCTCTCAAGCGGAGGAGGATGAGAGGAAATATC	6180
Db	5041	TGGCGCCCTAGTCTGGGGTCTGTGCGCAGCGATCTCGCTCGGACGCTGGGGCCAGG	5100	QY	6181	CGTTCCGCGGAGATCTCTGCGGAGTCTCAGGAAATTTCCCTCGAGGATGCCCATATGGGC	6240
QY	5101	GGAGGGGCTGTGCAGTGGATGAACCGGCTGATAGCGTTTCGCTTCGCGGGGTAAACAGT	5160				



Db	6181	CGTTCCGGCGAGATCCTGGGAGGTCCAGAAATTCCTTCGAGCGATGCCCATATGGGC	6240
Qy	6241	ACCCCGGATTACAAACCTCCACTGTTAGAGTCTCTGGAAGACCCCGACTACGTCCTCC	6300
Db	6241		6300
Qy	6301	AGTGGTACACGGGTGTCATTTGCCGCTGCGCAAGGCCCTCCGATACCACCTCCACGGAG	6360
Db	6301	AGTGGTACACGGGTGTCATTTGCCGCTGCGCAAGGCCCTCCGATACCACCTCCACGGAG	6360
Qy	6361	GAAGAGACGGTGTCTCTGTCAGAACTACCGTGTCTTCTGCTTGGCGGAGCTCGCCAC	6420
Db	6361	GAAGAGACGGTGTCTCTGTCAGAACTACCGTGTCTTCTGCTTGGCGGAGCTCGCCAC	6420
Qy	6421	AAAGACCTTCGGAGCTCCGAATCGTCGGCCGTCGACAGCGGACGCGCAACGCGCTCTCC	6480
Db	6421	AAAGACCTTCGGAGCTCCGAATCGTCGGCCGTCGACAGCGGACGCGCAACGCGCTCTCC	6480
Qy	6481	TGACCAAGCTTCGACGACGCGGACGCGGATCCGAGTTGAGTCTGTAATCTCTCCATGCC	6540
Db	6481	TGACCAAGCTTCGACGACGCGGACGCGGATCCGAGTTGAGTCTGTAATCTCTCCATGCC	6540
Qy	6541	CCCCCTTGAGGGGAGCGCGGGATCCCGATCTCAGCGACGGTCTTTGGTCTACCGTAAG	6600
Db	6541	CCCCCTTGAGGGGAGCGCGGGATCCCGATCTCAGCGACGGTCTTTGGTCTACCGTAAG	6600
Qy	6601	CGAGGAGCTAGTGAGACGTCGTCGCTGCTCGATGTCCTACACATGGACGACGCGCCT	6660
Db	6601	CGAGGAGCTAGTGAGACGTCGTCGCTGCTCGATGTCCTACACATGGACGACGCGCCT	6660
Qy	6661	GATCACGCCATGCGCTCGGAGGAAACAAAGCTGCCCATCAATGCACTGAGCAACTCTTT	6720
Db	6661	GATCACGCCATGCGCTCGGAGGAAACAAAGCTGCCCATCAATGCACTGAGCAACTCTTT	6720
Qy	6721	GCTCCGTACACAACTTGCTCTATGTCTAACAATCTCGAGGCGCAAGCCTCGCGCAGAA	6780
Db	6721	GCTCCGTACACAACTTGCTCTATGTCTAACAATCTCGAGGCGCAAGCCTCGCGCAGAA	6780
Qy	6781	GAAGGTACCTTTGACAGACTGAGGTCCTGGAGCACCCTACCGGACGTCGTCAAGGA	6840
Db	6781	GAAGGTACCTTTGACAGACTGAGGTCCTGGAGCACCCTACCGGACGTCGTCAAGGA	6840
Qy	6841	GATGAAGCGAAGCGTCCACAGTTAAGGCTAAACTTTCTATCCGTGGAGGAAGCCTGTAA	6900
Db	6841	GATGAAGCGAAGCGTCCACAGTTAAGGCTAAACTTTCTATCCGTGGAGGAAGCCTGTAA	6900
Qy	6901	GCTGACGCCCCACATTCGGCCAGATCTAAATTTGGCTATGGGCAAGAACGTCGCGAA	6960
Db	6901	GCTGACGCCCCACATTCGGCCAGATCTAAATTTGGCTATGGGCAAGAACGTCGCGAA	6960
Qy	6961	CCTATCCAGCAGCGGTTAACACATCCGCTCCGTGGAGGACTTGTGGAGACAC	7020
Db	6961	CCTATCCAGCAGCGGTTAACACATCCGCTCCGTGGAGGACTTGTGGAGACAC	7020
Qy	7021	TGAGACCAATTCACACACCATCATGGCAAAATAGAGTTTCTGCGTCCACACGA	7080
Db	7021	TGAGACCAATTCACACACCATCATGGCAAAATAGAGTTTCTGCGTCCACACGA	7080
Qy	7081	GAAGGGGGCGCAGGACGCTGCTATCTGATATCCAGATTTGGGGTTGCTGTGTG	7140
Db	7081	GAAGGGGGCGCAGGACGCTGCTATCTGATATCCAGATTTGGGGTTGCTGTGTG	7140
Qy	7141	CGAGAAATGGCCCTTTACGATGTGCTCCACCTCCCTCAGGCCGTGATGGCTCTTC	7200
Db	7141	CGAGAAATGGCCCTTTACGATGTGCTCCACCTCCCTCAGGCCGTGATGGCTCTTC	7200
Qy	7201	ATACGGATTCGAATCTCTCTGACACGCGGTGAGTCTCTGTGATGCTTGGAAAGC	7260
Db	7201	ATACGGATTCGAATCTCTCTGACACGCGGTGAGTCTCTGTGATGCTTGGAAAGC	7260
Qy	7261	GAAGAAATGCCCTATGGCTTCGATATGACACCGCGCTGTTTGACTCAACGGTCACTGA	7320
Db	7261	GAAGAAATGCCCTATGGCTTCGATATGACACCGCGCTGTTTGACTCAACGGTCACTGA	7320

Qy	7321	GAATGACATCCGTGTTGAGGAGTCAATCTACCAATGTTGTGTGACTTGGCCCCGAAAGCCAG	7380
Db	7321	GAATGACATCCGTGTTGAGGAGTCAATCTACCAATGTTGTGTGACTTGGCCCCGAAAGCCAG	7380
Qy	7381	ACAGGCCATAAGGTGCTCTCAGACAGCGGCTTTACATCGGGGGCCCCCTGACTAATTTCTAA	7440
Db	7381	ACAGGCCATAAGGTGCTCTCAGACAGCGGCTTTACATCGGGGGCCCCCTGACTAATTTCTAA	7440
Qy	7441	AGGGCAGAACTCCGGCTATCGCGGTGCGCGGAGCGGTGTACTGACACACAGCTGCGG	7500
Db	7441	AGGGCAGAACTCCGGCTATCGCGGTGCGCGGAGCGGTGTACTGACACACAGCTGCGG	7500
Qy	7501	TAATACCTTCACATGTACTTCAAGGCGCTCGCGCTGTGAGGTGCGAAAGCTCCAGGA	7560
Db	7501	TAATACCTTCACATGTACTTCAAGGCGCTCGCGCTGTGAGGTGCGAAAGCTCCAGGA	7560
Qy	7561	CTGCGAGATGCTGTATGCGGAGACGACTTGTCTGTATCTGTGAAGCGCGGGACCCA	7620
Db	7561	CTGCGAGATGCTGTATGCGGAGACGACTTGTCTGTATCTGTGAAGCGCGGGACCCA	7620
Qy	7621	AGAGGACGAGGCGAGCTACGGGCTTTCACGAGGCTATGACTAGATATCTTGCCTCCCTC	7680
Db	7621	AGAGGACGAGGCGAGCTACGGGCTTTCACGAGGCTATGACTAGATATCTTGCCTCCCTC	7680
Qy	7681	TGGGACCCCGCCCAACCCAGAAATACGACTTGGAGTTGATTAACATCATGCTCTCTCAATGT	7740
Db	7681	TGGGACCCCGCCCAACCCAGAAATACGACTTGGAGTTGATTAACATCATGCTCTCTCAATGT	7740
Qy	7741	GTGAGTGGCGACGATGATCTGGCAAAAGGGTGTACTATCTCACCGGTGACCCACCAC	7800
Db	7741	GTGAGTGGCGACGATGATCTGGCAAAAGGGTGTACTATCTCACCGGTGACCCACCAC	7800
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Db	7801	CCCCCTTGGCGGGCTGCGTGGGAGACACTAGACACTCCAGTCAATTCCTGGGTAGG	7860
Qy	7861	CAACATCATCTGATGTCGCCCCACCTTGTGGCAAGGATGATCTCTGATGACTCATTTCTT	7920
Db	7861	CAACATCATCTGATGTCGCCCCACCTTGTGGCAAGGATGATCTCTGATGACTCATTTCTT	7920
Qy	7921	CTCCATCTCTTCTAGCTCAGAAACACTTGAAGCCCTAGATTGTGAGTCTACCGGGC	7980
Db	7921	CTCCATCTCTTCTAGCTCAGAAACACTTGAAGCCCTAGATTGTGAGTCTACCGGGC	7980
Qy	7981	CTGTTACTCCATTGAGCCACTTGACCTACTCAGATCATTCAACGACTCCACGGCCTTAG	8040
Db	7981	CTGTTACTCCATTGAGCCACTTGACCTACTCAGATCATTCAACGACTCCACGGCCTTAG	8040
Qy	8041	CGCATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGGTGGCTTCATGCTCAG	8100
Db	8041	CGCATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGGTGGCTTCATGCTCAG	8100
Qy	8101	GAACTTGGGTACCGCCCTTGGAGTCTGGAGACATCGGGCCAGAGTGTCCGCGTAG	8160
Db	8101	GAACTTGGGTACCGCCCTTGGAGTCTGGAGACATCGGGCCAGAGTGTCCGCGTAG	8160
Qy	8161	GCTACTGTCCAGGGGGGGGGCTGCCACTTGTGCAAGTACTCTTCAACTGGGCGAGT	8220
Db	8161	GCTACTGTCCAGGGGGGGGGCTGCCACTTGTGCAAGTACTCTTCAACTGGGCGAGT	8220
Qy	8221	AAGGACCAAGCTCAAACTCACTCCAGTGGGTGCTCCAGTTGGATTTATCCAGCTG	8280
Db	8221	AAGGACCAAGCTCAAACTCACTCCAGTGGGTGCTCCAGTTGGATTTATCCAGCTG	8280
Qy	8281	GTTTGTGTGTGTTACAGCGGGGAGACATATATATCAGAGCTGTCTGCGCCGACCCCG	8340
Db	8281	GTTTGTGTGTGTTACAGCGGGGAGACATATATATCAGAGCTGTCTGCGCCGACCCCG	8340
Qy	8341	CTGGTTCACTGTGTGCTACTCTTCTGTTAGGGGTAGGCATCTATCTACTCCCAA	8400
Db	8341	CTGGTTCACTGTGTGCTACTCTTCTGTTAGGGGTAGGCATCTATCTACTCCCAA	8400

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QY 8461 TCCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 8520
Db 8456 -----TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 8510
QY 8521 TTCCCTTTTTTTTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 8580
Db 8511 TTTTCCCTTTTTTTTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 8570
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QY 8641 GATCAAGT 8648
Db 8631 GATCAAGT 8638

RESULT 5
US-10-789-355-25
; Sequence 25, Application US/10789355
; GENERAL INFORMATION:
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
; TITLE OF INVENTION: HEPATITIS C VIRUS
; FILE REFERENCE: 13/083
; CURRENT APPLICATION NUMBER: US/10/789,355
; PRIOR FILING DATE: 2004-02-27
; PRIOR FILING DATE: 2001-12-21
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,857
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 8638
; TYPE: DNA
; ORGANISM: HCV
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1802)...(8407)
US-10-789-355-25
;
Query Match 99.2%; Score 8577.2; DB 1; Length 8638;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 8609; Conservative 0; Mismatches 28; Indels 10; Gaps 1;

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482 TGATGCGCGCTGTTCCGGCTGTGAGCGCAGGGGCGCCGGTCTCTTTTGTCAAGACCGA 541
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QY 3362 GGCACAGTCTCTGGACCAAGCGGAGACGCTGGAAGCGGACTCGTCTGCTCGCACCGCT 3421  
DB |||||  
QY 3362 GGCACAGTCTCTGGACCAAGCGGAGACGCTGGAAGCGGACTCGTCTGCTCGCACCGCT 3421  
DB |||||  
QY 3422 ACGCTTCCGGGATCGGTGCAACGTCGTCATCAGAACATCGAGGAGGTGCTCTGTCAGC 3481  
DB |||||  
QY 3422 ACGCTTCCGGGATCGGTGCAACGTCGTCATCAGAACATCGAGGAGGTGCTCTGTCAGC 3481  
DB |||||  
QY 3482 ACTGGAGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACCATCAAGGGGGGAGG 3541  
DB |||||  
QY 3482 ACTGGAGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACCATCAAGGGGGGAGG 3541  
DB |||||  
QY 3542 CACTCATTTTCTGCAATTCGAAGAAGAAATGTGATGAGCTCGCCGCGAAGCTGTCCGC 3601  
DB |||||  
QY 3542 CACTCATTTTCTGCAATTCGAAGAAGAAATGTGATGAGCTCGCCGCGAAGCTGTCCGC 3601  
DB |||||  
QY 3602 CTCGACTCAATGCTGTAGCATATTTACGGGGCTTGAATGATCGGTATACCACTAGC 3661  
DB |||||

D	b	3602	CTCGGACTCAATGCTGTAGCATATTACCGGGGCTTGTATGATCTCGTCATACCAACTAGC	3661	Q	y	4742	CTGATGGCATTACAGCCTCTATACAGCCCGCTCAACACCCAAACATACCCCTCTCTGTTT	4801
Q	y	3662	GGAGAGTCAATTGCTGTAGCAACGGACGCTCTAATGACGGGCTTTACCGCGCATTTTCGAC	3721	D	b	4742	CTGATGGCATTACAGCCTCTATACAGCCCGCTCAACACCCAAACATACCCCTCTCTGTTT	4801
D	b	3662	GGAGAGTCAATTGCTGTAGCAACGGACGCTCTAATGACGGGCTTTACCGCGCATTTTCGAC	3721	Q	y	4802	AAACATCTCTGGGGGATGGGTGGCCGCCAACTTGTCTCTCCAGCGCTGCTCTCTGCTTTC	4861
Q	y	3722	TCAATGATTCAGCTGCAATACATGTGTCAACCGACAGTTCAGCTTCAAGCTTGGACCCGACC	3781	D	b	4802	AAACATCTCTGGGGGATGGGTGGCCGCCAACTTGTCTCTCCAGCGCTGCTCTCTGCTTTC	4861
D	b	3722	TCAATGATTCAGCTGCAATACATGTGTCAACCGACAGTTCAGCTTCAAGCTTGGACCCGACC	3781	Q	y	4862	GTAGGCGCGGCATCGCTGGAGCGCTGTGGACGATAGGCTTGGGAAGGTGCTTGTG	4921
Q	y	3782	TTCAACCATGAGACGACCGCTGCCAAGACGCGGTGTACGCTCGACGCGCGGAGGC	3841	D	b	4862	GTAGGCGCGGCATCGCTGGAGCGCTGTGGACGATAGGCTTGGGAAGGTGCTTGTG	4921
D	b	3782	TTCAACCATGAGACGACCGCTGCCAAGACGCGGTGTACGCTCGACGCGCGGAGGC	3841	Q	y	4922	GATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGCGCGCTCGTGGCCCTTTAAGGTCA	4981
Q	y	3842	AGGACTGGTAGGGCAGGATGGGCATTTACAGGTTTCTGACTCCAGAGAAACGGCCCTCG	3901	D	b	4922	GATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGCGCGCTCGTGGCCCTTTAAGGTCA	4981
D	b	3842	AGGACTGGTAGGGCAGGATGGGCATTTACAGGTTTGTGACTCCAGAGAAACGGCCCTCG	3901	Q	y	4982	AGCGCGAGATGCCCTCAACCGAGGACCTGTGTTAACTACTCCCTGCTATCTCTCCCT	5041
Q	y	3902	GGCATGTTCCGATTCCTCGGTTCTGTGCGAGTGTATGACGCGGGCTGTGCTTGGTACGAG	3961	D	b	4982	AGCGCGAGATGCCCTCAACCGAGGACCTGTGTTAACTACTCCCTGCTATCTCTCCCT	5041
D	b	3902	GGCATGTTCCGATTCCTCGGTTCTGTGCGAGTGTATGACGCGGGCTGTGCTTGGTACGAG	3961	Q	y	5042	GGCGCCCTAGTCGTGGGGTCTGTGGCAGCGATCTGCTTCGGGCTTTCGGGCTTTC	5101
Q	y	3962	CTCACGCCCGCAGACCTCAGTTAGGTTGCGGGCTTACCTAAACACACAGGGGTTGCC	4021	D	b	5042	GGCGCCCTAGTCGTGGGGTCTGTGGCAGCGATCTGCTTCGGGCTTTCGGGCTTTC	5101
D	b	3962	CTCACGCCCGCAGACCTCAGTTAGGTTGCGGGCTTACCTAAACACACAGGGGTTGCC	4021	Q	y	5102	GAGGGGGCTGTGCACTGGATGAAACCGGCTGTAGCGTTTCGCTTCGCGGGTAAACCACTC	5161
Q	y	4022	GTCTGCCAGACCATCTGGAGTTCTGGGAGAGGCTTTTACAGGCTCACCACATAGAC	4081	D	b	5102	GAGGGGGCTGTGCACTGGATGAAACCGGCTGTAGCGTTTCGCTTCGCGGGTAAACCACTC	5161
D	b	4022	GTCTGCCAGACCATCTGGAGTTCTGGGAGAGGCTTTTACAGGCTCACCACATAGAC	4081	Q	y	5162	TCCCCCAGCACAATGTGTGCTGAGACGACGCTGAGCAGCTGTCTCATCAGATCTCTCT	5221
Q	y	4082	GCCCATTTCTTGTCCAGACTAAGCAGGAGAGCAACTTCCCTTACCTGTGTAGCATAC	4141	D	b	5162	TCCCCCAGCACAATGTGTGCTGAGACGACGCTGAGCAGCTGTCTCATCAGATCTCTCT	5221
D	b	4082	GCCCATTTCTTGTCCAGACTAAGCAGGAGAGCAACTTCCCTTACCTGTGTAGCATAC	4141	Q	y	5222	AGTCTTACCATCACTCAGCTGCTGAGAGGCTTCCAGCTGGATCAACAGGACTCTCTCC	5281
Q	y	4142	CAGGCTACGGTGTGCGCAGGGCTCAGGCTCCACCTCCATCGTGGGACCAAAATGTGGA	4201	D	b	5222	AGTCTTACCATCACTCAGCTGCTGAGAGGCTTCCAGCTGGATCAACAGGACTCTCTCC	5281
D	b	4142	CAGGCTACGGTGTGCGCAGGGCTCAGGCTCCACCTCCATCGTGGGACCAAAATGTGGA	4201	Q	y	5282	AGCCATGCTCCGGCTCGTGGCTAAAGAGATGTTTGGGATTTGGGATTTGACGCTTGTG	5341
Q	y	4202	TGTCTCATAGGCTTAAGCCTACGCTGCAAGGCGCAACGCGCTGCTGTATAGGCTGGGA	4261	D	b	5282	AGCCATGCTCCGGCTCGTGGCTAAAGAGATGTTTGGGATTTGGGATTTGACGCTTGTG	5341
D	b	4202	TGTCTCATAGGCTTAAGCCTACGCTGCAAGGCGCAACGCGCTGCTGTATAGGCTGGGA	4261	Q	y	5342	GATTTCAAGACCTGGCTCCAGTCCAGTCTTCCCGCGATTTCCCGGAGTCCCTCTTCTTC	5401
Q	y	4262	GCGTTCAAAACGAGGTTACTACACACACCCCAATACCAATATACATCATGATGATG	4321	D	b	5342	GATTTCAAGGCTTGGCTCCAGTCCAGTCTTCCCGCGATTTCCCGGAGTCCCTCTTCTTC	5401
D	b	4262	GCGTTCAAAACGAGGTTACTACACACACCCCAATACCAATATACATCATGATGATG	4321	Q	y	5402	TCATGTCACGCTGGGTACAAAGGAGTCTGCGCGGGGACGCGATCATGCAAAACCACTGC	5461
Q	y	4322	TCGGCTGACCTGGAGTGTCTACGAGCACTGTGGTGTGTGTAGCGGAGTCTTACGAGCT	4381	D	b	5402	TCATGTCACGCTGGGTACAAAGGAGTCTGCGCGGGGACGCGATCATGCAAAACCACTGC	5461
D	b	4322	TCGGCTGACCTGGAGTGTCTACGAGCACTGTGGTGTGTGTAGCGGAGTCTTACGAGCT	4381	Q	y	5462	CCATGTGGAGCAGACATCAACCGGACATGTGAAAAAATGTTTCCATGAGGATCGTGGGCT	5521
Q	y	4382	CTGGCCGGTATTGCTTGAACAGGAGGAGTGTGCTATTGTTGGCAGGATCATCTTGTCC	4441	D	b	5462	CCATGTGGAGCAGACATCAACCGGACATGTGAAAAAATGTTTCCATGAGGATCGTGGGCT	5521
D	b	4382	CTGGCTGCGTATTGCTTGAACAGGAGGAGTGTGCTATTGTTGGCAGGATCATCTTGTCC	4441	Q	y	5522	AGGACCTGTAGTAAACAGCTGGGATGGAACATTTCCCATTTAACCGCTTACACCGGCCCC	5581
Q	y	4442	GGAAAGCGGCGCATCTTTCCGACAGGAGGAGTCTTTACCGGGAGTTCGATGAGATGGAA	4501	D	b	5522	AGGACCTGTAGTAAACAGCTGGGATGGAACATTTCCCATTTAACCGCTTACACCGGCCCC	5581
D	b	4442	GGAAAGCGGCGCATCTTTCCGACAGGAGGAGTCTTTACCGGGAGTTCGATGAGATGGAA	4501	Q	y	5582	TGCAAGCCTTCCCGCGCGCAAAATTTCTAGGGCTGTGGCGGGTGGCTGTGAGGAG	5641
Q	y	4502	GAGTGGCCTCACCTCCCTTACATCGAAACAGGGAATCAGCTCGCGGACCAATTCAAA	4561	D	b	5582	TGCAAGCCTTCCCGCGCGCAAAATTTCTAGGGCTGTGGCGGGTGGCTGTGAGGAG	5641
D	b	4502	GAGTGGCCTCACCTCCCTTACATCGAAACAGGGAATCAGCTCGCGGACCAATTCAAA	4561	Q	y	5642	TACGTGGAGGTTACCGGGTGGGGATTTTCCACTACGTGACGGGATGACCACTGACCAAC	5701
Q	y	4562	CAGAGGCAATCGGGTGTGTCGAAACAGCCACAGGAGGAGGCTGTGCTTCCCGTG	4621	D	b	5642	TACGTGGAGGTTACCGGAGTGGGGATTTTCCACTACGTGACGGGATGACCACTGACCAAC	5701
D	b	4562	CAGAGGCAATCGGGTGTGTCGAAACAGCCACAGGAGGAGGCTGTGCTTCCCGTG	4621	Q	y	5702	GTAAAGTGGCGGTTCAGGTTCCGGCCCCGGAATTTCTTACAGAGTGGATGGGGTCCGG	5761
Q	y	4622	GTGGAATCCAGTGGCGGACCTCGAAGCCTTCTGGGCGAAGCATATGTGGAATTTTATC	4681	D	b	5702	GTAAAGTGGCGGTTCAGGTTCCGGCCCCGGAATTTCTTACAGAGTGGATGGGGTCCGG	5761
D	b	4622	GTGGAATCCAGTGGCGGACCTCGAAGCCTTCTGGGCGAAGCATATGTGGAATTTTATC	4681	Q	y	5762	TTGCAAGGATCGCTCCAGGCTGCAACCCCTCTACGGGAGGAGGTCACTTCTCTGGTC	5821
Q	y	4682	AGCGGGATACAAATATTAGCAGGCTTGTCCACTCTGCTGGCAACCCCGGATAGCATCA	4741	D	b	5762	TTGCAAGGATCGCTCCAGGCTGCAACCCCTCTACGGGAGGAGGTCACTTCTCTGGTC	5821
D	b	4682	AGCGGGATACAAATATTAGCAGGCTTGTCCACTCTGCTGGCAACCCCGGATAGCATCA	4741					